

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 01:57:22 ; Search time 1844 Seconds
(without alignments)
7827.131 Million cell updates/sec

Title: US-09-019-441A-1_COPY_58_390

Perfect score: 333

Sequence: 1 cagctgtcccgactcagcc.....cccggttgacgctcctaggt 333

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 2933116

Minimum DB seq length: 0

Maximum DB seq length: 333

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_scs.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_scs.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	289.8	87.0	333	9	AB064024	AB064024 Homo sapi
2	289.8	87.0	333	9	HSJ399863	AJ399863 Homo sapi
3	288.2	86.5	333	9	AB064000	AB064000 Homo sapi
4	287.8	86.4	331	9	HSJ006162	AJ006162 Homo sapi
5	286.8	86.1	330	9	AF194592	AF194592 Homo sapi
6	286.8	86.1	330	9	AF194604	AF194604 Homo sapi
7	286.6	86.1	333	9	AB063978	AB063978 Homo sapi
8	286.6	86.1	333	9	HSJGLCVR	X95739 H.sapiens m
9	285.2	85.6	330	9	AF194579	AF194579 Homo sapi
10	285.2	85.6	330	9	AF194586	AF194586 Homo sapi
11	285.2	85.6	330	9	AF194587	AF194587 Homo sapi
12	285.2	85.6	330	9	AF194589	AF194589 Homo sapi
13	285.2	85.6	330	9	AF194605	AF194605 Homo sapi
14	285.2	85.6	330	9	AF194608	AF194608 Homo sapi
15	285.2	85.6	333	9	HSJ06676	U76676 Homo sapien
16	284.6	85.5	331	9	HSJ249377	AJ249377 Homo sapi
17	283.6	85.2	330	9	AF194595	AF194595 Homo sapi
18	283.6	85.2	330	9	AF194603	AF194603 Homo sapi
19	283.6	85.2	330	9	AF194607	AF194607 Homo sapi
20	283.4	85.1	333	9	HSJ84836	Z84836 H.sapiens g
21	282	84.7	330	9	AF194557	AF194557 Homo sapi
22	282	84.7	330	9	AF194596	AF194596 Homo sapi
23	282	84.7	330	9	AF194609	AF194609 Homo sapi
24	282	84.7	330	9	HSJ243109	AJ243109 Homo sapi
25	282	84.7	330	9	FUMIGLVJB	M80916 H.sapiens i
26	281.8	84.6	333	9	AB064017	AB064017 Homo sapi
27	281.4	84.5	333	9	HSJ496502	AJ496502 Homo sapi
28	280.8	84.3	333	6	AXL67727	AXL67727 Sequence
29	280.8	84.3	333	9	AF194540	AF194540 Homo sapi
30	280.4	84.2	330	9	AF194541	AF194541 Homo sapi
31	280.4	84.2	330	9	AF194543	AF194543 Homo sapi
32	280.4	84.2	330	9	AF194547	AF194547 Homo sapi
33	280.4	84.2	330	9	AF194548	AF194548 Homo sapi
34	280.4	84.2	330	9	AF194552	AF194552 Homo sapi
35	280.4	84.2	330	9	AF194553	AF194553 Homo sapi
36	280.4	84.2	330	9	AF194566	AF194566 Homo sapi
37	280.4	84.2	330	9	AF194571	AF194571 Homo sapi
38	280.4	84.2	330	9	AF194573	AF194573 Homo sapi
39	280.4	84.2	330	9	AF194580	AF194580 Homo sapi
40	280.4	84.2	330	9	AF194606	AF194606 Homo sapi
41	280.4	84.2	330	9	AY043162	AY043162 Homo sapi
42	279.8	83.9	331	9	AB063993	AB063993 Homo sapi
43	279.8	83.9	330	9	AF194555	AF194555 Homo sapi
44	278.8	83.7	330	9	AF194556	AF194556 Homo sapi
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ALIGNMENTS

RESULT 1
AB064024
LOCUS
DEFINITION
AB064024 Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:LI53.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

333 bp mRNA linear PRI 02-JUL-2002
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:LI53.
AB064024.1 GI:21669254
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,

SOURCE	variable region.
ORGANISM	Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Chapal,N., Chardes,T., Bresson,D., Pugnieri,M., Mani,J.C., Pau,B., Bouanani,M. and Peraldi-Koux,S.
TITLE	Thyroid peroxidase autoantibodies obtained from random single chain Fv libraries contain the same heavy/light chain combinations as occur in vivo
JOURNAL	Endocrinology 142 (11), 4740-4750 (2001)

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PUBMED
11606439
REFERENCE
2 (bases 1 to 333)
AUTHORS
Chapal N.
TITLE
Direct Submission
JOURNAL
Submitted (05-JAN-2000) Chapal N., Faculte de Pharmacie, CNRS
UMR9921, 15 avenue Charles Flahault, Montpellier 34060, FRANCE
FEATURES
location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="810"
/cell_type="Thyroid infiltrating B cells"
/clone_lib="pams library"
/rearranged
/country="France"
/note="Anti-Thyroid peroxidase scPv fragment isolated from
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CDS

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/db_xref="REFSEQ:LOC06678"
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APKLMIYDVNSRPGSVNRFSGSKSGNTASITISGLQAEADQYICSSYTSSSRVRFG
GGTKLTVLG"
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/gene="IGLV"
/product="immunoglobulin lambda chain variable region"

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Best Local Similarity 91.9%; Pred. No. 5.9e-74;
Matches 306; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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1 CAGTCTGCGCTGACTACGCCTGCCCTGTCTGGGTCTCTCTGACAGTCGATCACCATC 60

61 TCCGTGACTGSAACCAACGCGATGAGTTGTGTGTATTAACATATGTCCTCTGTATCCACAC 120
61 TCCGTGACTGSAACCAACGAGTGAGTTGGTGGTTATTAACATATGTCCTCTGTATCCACAG 120

121 CACCACGCAAGCCCCCAAACTCATGATTATATGATGTGCTAAGCGGGCTCTAGGGGTC 180
121 CACCACGCAAGCCCCCAAACTCATGATTATTAATGTGACTAATCGGCTCTAGGGGTT 180

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181	TCTGATCGCTTCTCTGCTCCAAAGTCGGCAACGCGCTCCCTCGACCATCTCGGGTC	240
181	TCTAAATCGCTTCTCTGCTCCAAAGTCGGCAACGCGCTCCCTCGACCATCTCTGGGCTC	240
241	CAGGCTCAGACGAGGCTGATTATTA	300
241	CAGGCTGAGACGAGGCTGATTATTA	300
301	TTCGGAAGACGGACCCGGTTGACCGTCTTAGGT	333

181 TCTAATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 240

241 CAGGCTGAGGACGAGGCTGATTACTGTTGTTTCATATACCAACGAGTACCTTTGTTA 300

241 CAGGCTGAGGACGAGGCTGATTACTGAGCTCATATACAGCAGCATTATGTC 300

301 TTCCGAAGAGGAGCCCGGTTGACCGTCTCTAGGT 333

301 TTCCGAAGTGGACCAAGGTCACCGTCTCTAGGT 333

RESULT 4

LOCUS HSA006162 331 bp mRNA linear PRI 20-JUL-1999

DEFINITION Homo sapiens mRNA for variable region of Ig light chain, rearrangement of BC2 cell line).

ACCESSION AJ006162

VERSION AJ006162.1 GI:5566504

KEYWORDS immunoglobulin; light chain; variable region.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 Fais, P., Gaidano, G., Capello, D., Ghoghini, A., Ghiotto, F., Roncella, S., Carbone, A., Chiorazzi, N. and Ferrarini, M. Immunoglobulin V region gene use and structure suggest antigen selection in AIDS-related primary effusion lymphomas Leukemia 13 (7), 1093-1099 (1999)

JOURNAL MEDLINE 99326013

PUBMED 10400426

REFERENCE 2 (bases 1 to 331)

AUTHORS Fais, P.

TITLE Direct Submission

JOURNAL Submitted (14-MAY-1998) Fais P., Clinical Immunology, Istituto Nazionale per la Ricerca sul Cancro, L.go R. Benzi 10, 16132, ITALY

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/cell_line="BC2"

/cell_type="B lymphocyte derived lymphoma"

/rearranged

/note="derived from AIDS-related primary effusion lymphoma"

1..331

/gene="VL2a2 gene"

1..330

/gene="VL2a2 gene"

/product="variable region of immunoglobulin light chain"

ORIGIN

Query Match 86.4%; Score 287.8; DB 9; Length 331;

Best Local Similarity 91.8%; Pred. No. 2.3e-73;

Matches 304; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCCGTCAACATC 60

DB 1 CAGTCTGCCCTGATCTAGCCCTGCTCGTGTCTGGGTCTCTGGACAGTCCGTCAACATC 60

QY 61 TCCTGCGCTGGAACACGAGGATGAGTTGGTGGTTATTAATCTATGTTCTCTGTGACCAAC 120

DB 61 TCCTGCGCTGGAACACGAGGATGAGTTGGTGGTTATTAATCTATGTTCTCTGTGACCAAC 120

QY 121 CACCCAGGCAAGGCCCCCAACTCATGATTATGATGTCGCTAAGCGGGCTCAGGGGTC 180

DB 121 CACCCAGGCAAGGCCCCCAACTCATGATTATGATGTCGCTAAGCGGGCTCAGGGGTC 180

QY 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 240

181 TCTAATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 240

301 TTCCGGGAGGACCAAGCTGACCGTCTCTAGGT 333

AB064000 333 bp mRNA linear PRI 02-JUL-2002

LOCUS Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ region, partial cds, clone:LI29.

DEFINITION

ACCESSION AB064000

VERSION AB064000.1 GI:21669206

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y. Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics

AUTHORS Unpublished

JOURNAL Kurosawa, Y.

REFERENCE 2 (bases 1 to 333)

TITLE Direct Submission

JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Kutsukake-cho, Toyokake 470-1192, Japan

COMMENT (E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)

Please visit our web site

URL: <http://www.fujita-hu.ac.jp/immunity/>.

FEATURES

Location/Qualifiers

1..333

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="AIMS4"

/note="mixture of tissues: tonsils, umbilical cords, peripheral blood and bone marrow"

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/gene="IGL"

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/gene="IGL"

/codon_start=1

/product="immunoglobulin lambda light chain VLJ region"

/protein_id="BAC01628.1"

/db_xref="GI:21669207"

/translation="QSAUTQPASVSGSPQISITICTGTSSDVGGYNYVSWVOHPGKAPKMLYDVSKRPSGVSNRPSGSKSNTASLTISLQAEADRDYICSSYTSSTVFGTGTKYTVLG"

ORIGIN

Query Match 86.5%; Score 288.2; DB 9; Length 333;

Best Local Similarity 91.6%; Pred. No. 1.7e-73;

Matches 305; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCCGTCAACATC 60

DB 1 CAGTCTGCCCTGACTCAGCCTCCCTCCCGGTCTCTGGGTCTCTGGACAGTCCGTCAACATC 60

QY 61 TCCTGCACTGGAACACGAGGATGAGTTGGTGGTTATTAATCTATGTTCTCTGTGACCAAC 120

DB 61 TCCTGCACTGGAACACGAGGATGAGTTGGTGGTTATTAATCTATGTTCTCTGTGACCAAC 120

QY 121 CACCCAGGCAAGGCCCCCAACTCATGATTATGATGTCGCTAAGCGGGCTCAGGGGTC 180

DB 121 CACCCAGGCAAGGCCCCCAACTCATGATTATGATGTCGCTAAGCGGGCTCAGGGGTC 180

QY 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 240

Db	181	TCCTAATCGCTTCCTCTGGGCTCAAGCTCTGGGCAACAGCGGCTCCCTCTGACCATCTCTCGGBCTC	240
Qy	241	CAGGCTGAGGAGCGAGGCTGATATTACTGTGTGTTCATATACACACGAGTAGCACTTTGGTA	300
Db	241	CAGGCTGAGGAGCGAGGCTGATATTACTGTGTGTTCATATACACACGAGTAGCACTTTGGTA	300
Qy	301	TTCCGAGAGGAGGACCGGTTGACCGTCCTA	330
Db	301	TTCCGCGGAGGGAGCCAAAGTGACCGTCCTA	330

RESULT 7					
AB063398	AB063398	Homo sapiens IGL mRNA for immunoglobulin lambda light chain VJLJ region, partial cds, clone:L107.	333 bp	mRNA	linear PRI 02-JUL-2002
LOCUS	DEFINITION				
	ACCESSION	AB063398			
	VERSION	AB063398.1	GI:21669162		

RECORDS	SOURCE	ORGANISM
	Homo sapiens (human)	
	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homidae; Homo.	
REFERENCE		
1		
AUTHORS		
	1. Akahori, Y., Iba, Y., Morino, K., Shinchara, M., Hirano, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.	
TITLE		
	Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional	

genomics.
Unpublished
2 (bases 1 to 333)
Kurosawa, Y.
Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kusumake-cho, Toyosake 470-1192, Japan
(E-mail: kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL: <http://www.fujita-hu.ac.jp/immunity/>.

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FEATURES             source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L107"
/clone_lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
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/gene="IGL"
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/protein_id="BAC01606.1"
/db_xref="GI:21669163"
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ORIGIN
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Best Local Similarity 91.3%; Pred. No. 5.le-73;
Matches 304; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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Db                  1   CAGTCTGCCCTGACTCAGCTCGCTCAGTCTCGGGTCTCTCTGGACAGTCAGTCACCACATC 60

QY    61  TCCTGCATCTGGAACACAGCGATGAGTTGGTGGTTTAACTATGTCTCTCTGGTACCAAAC 120
Db                  61  TCCTGCATCTGGAAACACAGAGTGAATTGGTGGTTTAACTATGTCTCTCTGGTACCAAAC 120

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Best Local Similarity 91.3%; Pred. No. 5.1e-73;
Matches 304; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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Db 1 CAGTCTCCCGGACTCAGCCTCCCTCTGTGTCTGGGCTCTCTGGACAGTGGGTCAACATC 60
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Qy 61 TCTGCACTGGACAGGAGTGGTGGTGTATTAATATGTCCTCTGGTACCAACAC 120
    |||||
Db 61 TCTGCACTGGACAGGAGTGGTGGTGTATTAATATGTCCTCTGGTACCAACAG 120
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Qy 121 CACCCAGGCAAGCCCAAACTCATGATTATGATCGCTAAGCGGGCTCAGGGGTC 180
    |||||
Db 121 CACCCAGGCAAGCCCAAACTCATGATTATGATCGCTAAGCGGGCTCAGGGGTC 180
    |||||
Qy 181 TCTGATCGCTTCTGTGCTCCAGTCTGGCAACAGCGCTCCCTGACCAATCTCTGGGTC 240
    |||||
Db 181 TCTGATCGCTTCTGTGCTCCAGTCTGGCAACAGCGCTCCCTGACCAATCTCTGGGTC 240
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Qy 241 CAGGCTGAGGAGTGGTGGTGTATTAATATGTCCTATACCAACAGTGGTGT 300
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Qy 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTAGGT 333
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Db 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTAGGT 333
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RESULT 9
AF194579
LOCUS 330 bp mRNA linear PRI 10-JAN-2000
DEFINITION Homo sapiens clone 1034 immunoglobulin lambda light chain variable
region mRNA, partial cds.
ACCESSION AF194579
VERSION AF194579.1 GI:6643156
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 330)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ignatovich, O., Tomlinson, I.M., Popov, A.V., Bruggemann, M. and
Winter, G.
TITLE Dominance of intrinsic genetic factors in shaping the human
immunoglobulin Vlambda repertoire
J. Mol. Biol. 294 (2), 457-465 (1999)
PUBMED 10610771
REFERENCE 2 (bases 1 to 330)
AUTHORS Ignatovich, O., Tomlinson, I.M., Popov, A.V., Bruggemann, M. and
Winter, G.
TITLE Direct Submission
Submitted (13-OCT-1999) Laboratory of Molecular Biology, MRC, Hills
Road, Cambridge CB2 2QH, UK
FEATURES
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/mol_type="mRNA"
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/clone="1034"
/notes="from the spleen of a transgenic mouse carrying a
380kb region of human Ig lambda locus DNA"
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region"
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GGTKLTVL"

CDS
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region"
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GGTKLTVL"

ORIGIN
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Query Match 85.6%; Score 285.2; DB 9; Length 330;
Best Local Similarity 91.5%; Pred. No. 1.3e-72;
Matches 302; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Db 1 CAGTCTCCCGGACTCAGCCTCCCTCTGTGTCTGGGCTCTCTGGACAGTGGGTCAACATC 60
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Qy 61 TCTGCACTGGACAGGAGTGGTGGTGTATTAATATGTCCTCTGGTACCAACAC 120
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Db 61 TCTGCACTGGACAGGAGTGGTGGTGTATTAATATGTCCTCTGGTACCAACAG 120
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Db 181 TCTGATCGCTTCTGTGCTCCAGTCTGGCAACAGCGCTCCCTGACCAATCTCTGGGTC 240
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Qy 241 CAGGCTGAGGAGTGGTGGTGTATTAATATGTCCTATACCAACAGTGGTGT 300
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Db 241 CAGGCTGAGGAGTGGTGGTGTATTAATATGTCCTATACCAACAGTGGTGT 300
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Db 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTAGGT 330
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RESULT 10
AF194586
LOCUS 330 bp mRNA linear PRI 10-JAN-2000
DEFINITION Homo sapiens clone 1233 immunoglobulin lambda light chain variable
region mRNA, partial cds.
ACCESSION AF194586
VERSION AF194586.1 GI:6643170
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 330)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ignatovich, O., Tomlinson, I.M., Popov, A.V., Bruggemann, M. and
Winter, G.
TITLE Dominance of intrinsic genetic factors in shaping the human
immunoglobulin Vlambda repertoire
J. Mol. Biol. 294 (2), 457-465 (1999)
PUBMED 10610771
REFERENCE 2 (bases 1 to 330)
AUTHORS Ignatovich, O., Tomlinson, I.M., Popov, A.V., Bruggemann, M. and
Winter, G.
TITLE Direct Submission
Submitted (13-OCT-1999) Laboratory of Molecular Biology, MRC, Hills
Road, Cambridge CB2 2QH, UK
FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1233"
/notes="from the spleen of a transgenic mouse carrying a
380kb region of human Ig lambda locus DNA"
<1..>330
/codon_start=1
/product="immunoglobulin lambda light chain variable
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ORIGIN
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Query Match 85.6%; Score 285.2; DB 9; Length 330;
Best Local Similarity 91.5%; Pred. No. 1.3e-72;
Matches 302; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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QY 301 TTCGGAAGAGGACCCGGTTCACGCTCCTA 330
DB 301 TTCGGAAGAGGACCCGGTTCACGCTCCTA 330

RESULT 11
AF194587
LOCUS
DEFINITION Homo sapiens clone 1302 immunoglobulin lambda light chain variable region mRNA, partial cds.
ACCESSION AF194587
VERSION AF194587.1 GI:6643172
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
AUTHORS Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and Winter,G.
TITLE Dominance of intrinsic genetic factors in shaping the human immunoglobulin Vlambda repertoire
J. Mol. Biol. 294 (2), 457-465 (1999)
MEDLINE 20079509
PUBMED 10610771
REFERENCE 2 (bases 1 to 330)
AUTHORS Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and Winter,G.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-1999) Laboratory of Molecular Biology, MRC, Hills Road, Cambridge CB2 2QH, UK
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Query Match 85.6%; Score 285.2; DB 9; Length 330;
Best Local Similarity 91.5%; Pred. No. 1.3e-72;
Matches 302; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGCTGGTCTCTGGACAGTCTGACCATC 60
DB 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGCTGGTCTCTGGACAGTCTGACCATC 60
QY 61 TCCTGCACTGGAACCCAGGATGACCTTGGTGTATTAACATGCTCTCGTACCAAC 120
DB 61 TCCTGCACTGGAACCCAGGATGACCTTGGTGTATTAACATGCTCTCGTACCAAC 120
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DB 121 CACCCAGGCAAGCCCAACTCATGATTTATGATGCTAGCGGCTTCAGGGGTC 180
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DB 301 TTCGGAAGAGGACCCGGTTCACGCTCCTA 330

RESULT 12
AF194589
LOCUS
DEFINITION Homo sapiens clone 1343 immunoglobulin lambda light chain variable region mRNA, partial cds.
ACCESSION AF194589
VERSION AF194589.1 GI:6643176
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
AUTHORS Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and Winter,G.
TITLE Dominance of intrinsic genetic factors in shaping the human immunoglobulin Vlambda repertoire
J. Mol. Biol. 294 (2), 457-465 (1999)
MEDLINE 20079509
PUBMED 10610771
REFERENCE 2 (bases 1 to 330)
AUTHORS Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and Winter,G.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-1999) Laboratory of Molecular Biology, MRC, Hills Road, Cambridge CB2 2QH, UK
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Query Match      85.6%; Score 285.2; DB 9; Length 330;
Best Local Similarity 91.5%; Pred. No. 1.3e-72;
Matches 302; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGCAGTCAGCCCTCCCTCTGTCTGTGGTCTCTCGACAGTCGGTCACCATC 60
Db 1 CAGTCTGCCCTGACTCAGCGCTGCCCTCCGCTGTCTGGTCTCTCGACAGTCGATCACCATC 60
Qy 61 TCCTGCACTGGAAACAGAGGAGTGAAGTGGTGGTGAATTAATATGTTCTCTGTTACCAACAC 120
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Qy 121 CACCCAGGCAAGAGCCGCCAACTCATGATTTATGATGTTCTGCTAAGCGGGCTCAGGGGTC 180
Db 121 CACCCAGGCAAGAGCCGCCAACTCATGATTTATGATGTTCTGCTAAGCGGGCTCAGGGGTC 180
Qy 181 TCCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240
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Qy 241 CAGGCTGAGGACGAGCGCTGATTTACTGTTTTCATATACAAACAGTAGCACTTTGTTA 300
Db 241 CAGGCTGAGGACGAGCGCTGATTTACTGTTTTCATATACAAACAGTAGCACTTTGTTA 300
Qy 301 TTCGGAAGAGGACCGGCTTGACCGTCTTA 330
Db 301 TTCGCGGAGGAGCAACAGCTGACCGTCTTA 330

RESULT 15
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LOCUS Homo sapiens clone BY-12LC Igm light chain variable region mRNA,
partial cds.
U76676
U76676.1 GI:1673590
ORIGIN
Query Match      85.6%; Score 285.2; DB 9; Length 330;
Best Local Similarity 91.5%; Pred. No. 1.3e-72;
Matches 302; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGCAGTCAGCCCTCCCTCTGTCTGTGGTCTCTCGACAGTCGGTCACCATC 60
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Qy 61 TCCTGCACTGGAAACAGAGGAGTGAAGTGGTGGTGAATTAATATGTTCTCTGTTACCAACAC 120
Db 61 TCCTGCACTGGAAACAGAGGAGTGAAGTGGTGGTGAATTAATATGTTCTCTGTTACCAACAG 120
Qy 121 CACCCAGGCAAGAGCCGCCAACTCATGATTTATGATGTTCTGCTAAGCGGGCTCAGGGGTC 180
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GGTKLTVL"
ORIGIN
Query Match      85.6%; Score 285.2; DB 9; Length 330;
Best Local Similarity 91.5%; Pred. No. 1.3e-72;
Matches 302; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGCAGTCAGCCCTCCCTCTGTCTGTGGTCTCTCGACAGTCGGTCACCATC 60
Db 1 CAGTCTGCCCTGACTCAGCGCTGCCCTCCGCTGTCTGGTCTCTCGACAGTCGATCACCATC 60
Qy 61 TCCTGCACTGGAAACAGAGGAGTGAAGTGGTGGTGAATTAATATGTTCTCTGTTACCAACAC 120
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Qy 121 CACCCAGGCAAGAGCCGCCAACTCATGATTTATGATGTTCTGCTAAGCGGGCTCAGGGGTC 180
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Qy 181 TCCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240
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Qy 241 CAGGCTGAGGACGAGCGCTGATTTACTGTTTTCATATACAAACAGTAGCACTTTGTTA 300
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Db 301 TTCGCGGAGGAGCAACAGCTGACCGTCTTA 330

Search completed: June 19, 2004, 04:01:33
Job time : 1847 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using **sw** model

Run on: June 19, 2004, 01:55:31 ; Search time 276 Seconds
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Title: US-09-019-441a-1_COPY_58_390

Perfect score: 333

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 4156560

Minimum DB seq length: 0

Maximum DB seq length: 333

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: Geneseqm2001as:*
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- 8: Geneseqm2003bs:*
- 9: Geneseqm2003cs:*
- 10: Geneseqm2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	280.8	84.3	333	4	AH42407 Nucleotid
2	280.8	84.3	333	4	AH42401 Nucleotid
3	275.8	82.8	330	6	ABX00191 Mouse DNA
4	275.8	82.8	330	6	ABK71397 Thrombopo
5	275.4	82.7	333	2	AAT10327 Human ant
6	275.4	82.7	333	2	AAZ31655 Coding se
7	273.8	82.2	333	2	AAZ31654 Coding se
8	270.8	81.3	330	4	AA033477 DNA encod
9	269.2	80.8	330	4	AA033520 DNA encod
10	265.8	79.8	333	2	AQ55659 Monoclonal
11	262.8	78.9	330	8	ACC85452 Human gly
12	248.4	74.6	327	4	Aaf58706 Huntingtin
13	243.6	73.2	330	6	AAD46293 Human KDR
14	243.6	73.2	330	7	ABT23328 VEGF bind
15	243.6	73.2	330	9	ADD24421 Human lig
16	243.6	73.2	330	9	ADD80798 Human clo
17	242.7	72.7	330	6	AAD46298 Human KDR
18	242.7	72.7	330	7	ABT23333 VEGF bind
19	242.7	72.7	330	9	ADD24431 Human lig
20	242.7	72.7	330	9	ADD80808 Human KDR
21	239.6	72.0	324	5	AAH68682 Human ant
22	239.6	72.0	324	8	ACD45346 Anti-Rh(D
23	239.2	71.8	300	3	AAA52443 Wild-type

24	237	71.2	294	4	ABA70898 Human foe
25	237	71.2	294	4	AAI51083 Probe #19
26	237	71.2	294	4	ABA37341 Probe #15
27	237	71.2	294	4	AAK45127 Human bon
28	237	71.2	294	4	AAK19166 Human bra
29	237	71.2	294	4	ABS44798 Human liv
30	237	71.2	294	6	ABS19377 Human gen
31	234.4	70.4	300	3	AA52446 High affi
32	230	69.1	279	3	AA56720 HuIgIambd
33	228	68.5	300	3	AA52444 Streptativ
34	227.4	68.3	333	4	AA03506 DNA encod
35	220.8	66.3	283	3	AAA56719 Human Ig
36	212.4	63.8	279	3	AAA56724 HuIgIambd
37	211.2	63.4	283	3	AAA56723 Human Ig
38	208.8	62.7	312	5	AAH68683 Human ant
39	208.8	62.7	312	8	ACD45347 Anti-Rh(D
40	202	60.7	330	8	ADA99167 DNA encod
41	201.8	60.6	330	4	AA03527 DNA encod
42	201.4	60.5	331	4	AAI68771 Human ant
43	198.6	59.6	330	4	AA03458 DNA encod
44	198.4	59.6	333	4	AA03485 DNA encod
45	197	59.2	330	4	AA03529 DNA encod

ALIGNMENTS

RESULT 1

AAH42407
ID AAH42407 standard; DNA; 333 BP.

AC AAH42407;

DT 01-OCT-2001 (first entry)

DS Nucleotide sequence of variable light chain fragment of clone G102.

XX Antibody; light chain; VL; amyloid protein; blood brain barrier;
XX endothelial cell; brain cell antigen; inflammation; adhesion molecule;
XX transferrin receptor; neurological disease; Alzheimer's disease;
XX prion disease; AIDS-related dementia; epilepsy; brain injury; ss.

OS Homo sapiens.

XX WO200144300-A2.

XX 21-JUN-2001.

XX 27-NOV-2000; 2000WO-GB004501.

XX 13-DEC-1999; 99US-0170599P.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Webster C, Osbourn J, Ward G, Miller K;

XX WPI: 2001-398131/42.

XX P-PSDB; AAG62963.

XX Mixture or panel of antibodies for selecting specific binding members
XX that cross the blood brain barrier, for use in delivering different
XX molecules and treating neurological diseases.

XX Disclosure; Page 106; 109pp; English.

XX The present sequence encodes an antibody variable light chain (VL)
XX fragment. The fragment is used to produce a mixture or panel of 5
XX different specific binding members, each comprising an antibody VH and/or
XX VL variable domain and capable, when displayed on the surface of
XX filamentous bacteriophage particles or in the case of a specific binding
XX member comprising the D5 VH and/or VL variable domain when bound to human
XX serum amyloid protein, to pass through a mammalian blood brain barrier
XX (BBB). The panel is useful for the selection of specific binding members

CC with a desired property such as ability to cross BBB, ability to bind
CC endothelial cells or other brain cell antigen, ability to bind areas of
CC inflammation in the brain or BBB breakdown or ability to bind
CC intracellular adhesion molecules and to bind transferrin receptor. The
CC antibodies are useful in diagnosis, prophylaxis and treatment of human or
CC animal body, including neurological diseases, such as Alzheimer's
CC disease, prion disease, AIDS-related dementia, epilepsy and traumatic
CC brain injury and any diseases involving inflammation occurring within the
CC brain or central nervous system
XX
SQ Sequence 333 BP; 72 A; 99 C; 86 G; 76 T; 0 U; 0 Other;

Mixture or panel of antibodies for selecting specific binding members
 that cross the blood brain barrier, for use in delivering different
 molecules and treating neurological diseases.
 Disclosure; Page 103; 109pp; English.
 The present sequence encodes an antibody variable light chain (VL)
 fragment. The fragment is used to produce a mixture or panel of 5
 different specific binding members, each comprising an antibody VH and/or
 VL variable domain and capable, when displayed on the surface of
 filamentous bacteriophage particles or in the case of a specific binding
 member comprising the DS VH and/or VL variable domain when bound to human
 serum amyloid protein, to pass through a mammalian blood brain barrier
 (BBB). The panel is useful for the selection of specific binding members
 with a desired property such as ability to cross BBB, ability to bind
 endothelial cells or other brain cell antigen, ability to bind areas of
 inflammation in the brain or BBB breakdown or ability to bind
 intracellular adhesion molecules and to bind transferrin receptor. The
 antibodies are useful in diagnosis, prophylaxis and treatment of human or
 animal body, including neurological diseases, such as Alzheimer's
 disease, prion disease, AIDS-related dementia, epilepsy and traumatic
 brain injury and any diseases involving inflammation occurring within the
 brain or central nervous system
 Sequence 333 BP; 71 A; 99 C; 87 G; 76 T; 0 U; 0 Other;

XX PD 25-APR-2002.
XX PF 22-OCT-2001; 2001WO-JP009260.
XX PR 20-OCT-2000; 2000JP-00321821.
XX PR 20-OCT-2000; 2000JP-00321822.
XX PR 12-MAR-2001; 2001WO-JP001912.
XX PR 17-APR-2001; 2001WO-JP003288.
XX PR 12-SEP-2001; 2001JP-00277314.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Fukushima N, Tsuchiya M, Uno S, Ohtomo T, Yabuta N, Tsunoda H;
XX DR WPI; 2002-682599/73.
XX DR P-FSDS; ABG97830.
XX PT Modified single chain multimeric Fv antibody acting as a signal
XX PT transduction agonist for treatment of inflammatory hormonal and blood
XX PT disorders and cancer.
XX PS Example 8; Page 202; 217pp; Japanese.
XX CC The invention relates to a new modified single chain Fv antibody
XX CC containing at least two heavy chain variable domains and at least two
XX CC light chain variable domains from the same or different monoclonal
XX CC antibodies and which is an agonist for crosslinking a molecule at the
XX CC cell surface or within the cell and thereby transducing a signal into the
XX CC cell. Also include are the DNA encoding the antibody, animal cells and
XX CC microorganisms transformed by and expressing the DNA, the preparation of
XX CC the antibodies by culture of the transformed cells, drug compositions
XX CC containing the antibodies and an assay method for the agonist activity of
XX CC the antibodies by contacting the antibodies with cells expressing the
XX CC relevant cell surface or internal molecule. The antibodies are useful for
XX CC treatment and prevention of cancer, inflammatory disease, hormonal
XX CC disorders including diabetes, autoimmune disease, leukaemia, a DNA
XX CC dysendocrinism and blood disorders. The present invention is a DNA
XX CC sequence encoding an antibody of the invention or a fragment thereof
XX SQ Sequence 330 BP; 73 A; 100 C; 83 G; 74 T; 0 U; 0 Other;
Query Match 82.8%; Score 275.8; DB 6; Length 330;
Best Local Similarity 90.2%; Pred. No. 1.8e-76;
Matches 295; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Qy 4 TCTGCCCGACTCAGCCTCCCTCTGTCTGGGTCTCTCTGGACAGTGGTCAACCATCTCC 63
Db 4 TATGTGCTGACTCGACCCACCTCGGTGTCTGGGTCTCTCTGGACAGTGGTCAACCATCTCC 63
Qy 64 TGCACCTGGAACCCAGGATGACGTTGGTGGTTATTAACATATGCTCTCTGTACCAACAC 123
Db 64 TGCACCTGGAACCCAGGATGACGTTGGTGGTTATTAACATATGCTCTCTGTACCAACAC 123
Qy 124 CCAGGCAAGCCGCCAAACTCATGATTTATGATGCTCGCTAAGCGGCTCAGGGGTCTCT 183
Db 124 CCAGGCAAGCCGCCAAACTCATGATTTATGAGGGCAGTAAACGGCCCTCAGGGGTCTCT 183
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Db 184 AATCGCTTCTCTGGCTCCAGTCTGGCAACACCGCCCTCTCTGACCATCTCTGGGCTCCAG 243
Qy 244 GCTGAGACGAGGCTGATTTACTTGTGTTTATATACCAACAGTACGACTTCTGTTATTC 303
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Db 304 GCGGAGGGAGCCAGCTGACCGTCTTA 330
RESULT 4
ABX71397

ID XX ABX71397 standard; DNA; 330 BP.
XX AC ABX71397;
XX DT 30-JUL-2002 (first entry)
XX DE Thrombopoietin (TPO) agonist antibody associated polynucleotide #15.
XX KW Modified antibody; thrombopoietin; TPO; agonist; TPO receptor;
XX KW platelet reduction-associated blood disease; thrombocytopenia;
XX KW cancer chemotherapy; leukaemia; signal transduction; ds.
XX OS Mus sp.
XX PI WO200233072-A1.
XX PD 25-APR-2002.
XX PF 22-OCT-2001; 2001WO-JP009259.
XX PR 20-OCT-2000; 2000JP-00321821.
XX PR 17-APR-2001; 2001WO-JP003288.
XX PR 12-SEP-2001; 2001JP-00277314.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Tsuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;
XX DR WPI; 2002-383513/41.
XX CC Degraded thrombopoietin agonist antibodies containing H and L chain V
XX CC domains of monoclonal antibody, useful in preventives and/or remedies for
XX CC blood diseases, thrombopenia following cancer chemotherapy or leukemia.
XX PS Example 8; Page 198-199; 213pp; Japanese.
XX CC The invention describes a modified antibody comprising at least 2 heavy
XX CC chain variable domains and 2 or more light chain variable domains of an
XX CC antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing
XX CC the TPO receptor to crosslink. The antibodies are useful in preventives
XX CC and/or remedies for platelet reduction-associated blood diseases,
XX CC thrombocytopenia following cancer chemotherapy or leukaemia. The antibody
XX CC can act as a TPO signal transduction agonist by transducing a signal into
XX CC cells by crosslinking a TPO receptor to exert TPO agonism. This sequence
XX CC represents thrombopoietin (TPO) agonist antibody associated
XX CC polynucleotide used in the creation of the modified antibody described in
XX CC the invention
XX SQ Sequence 330 BP; 73 A; 100 C; 83 G; 74 T; 0 U; 0 Other;
Query Match 82.8%; Score 275.8; DB 6; Length 330;
Best Local Similarity 90.2%; Pred. No. 1.8e-76;
Matches 295; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Qy 4 TCTGCCCGACTCAGCCTCCCTCTGTCTGGGTCTCTCTGGACAGTGGTCAACCATCTCC 63
Db 4 TATGTGCTGACTCGACCCACCTCGGTGTCTGGGTCTCTCTGGACAGTGGTCAACCATCTCC 63
Qy 64 TGCACCTGGAACCCAGGATGACGTTGGTGGTTATTAACATATGCTCTCTGTACCAACAC 123
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Db 244 GCTGAGACGAGGCTGATTTACTTGTGTTTATATACCAACAGTACGACTTCTGTTATTC 303

QY 304 GGAAGAGGACCCGGTTGACCGTCTTA 330
 DB 304 GGCAGGAGGACCAAGCTGACCGTCTTA 330

RESULT 5
 ID AAT10327 standard; cDNA to mRNA; 333 BP.
 AC AAT10327;
 XX
 XX 16-OCT-2003 (revised)
 DT 18-JUL-1996 (first entry)
 XX
 XX Human anti-Pseudomonas aeruginosa type B antibody VL region cDNA.
 DE Human; immunoglobulin; IgM; lambda light chain; variable region;
 KW lipopolysaccharide; LPS; antigen; Pseudomonas aeruginosa; type B;
 KW monoclonal antibody; 88.
 XX
 XX Homo sapiens; (cell line MP-5097).
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 XX Key Location/Qualifiers
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 FT /note= "coding region does not include start or stop
 FT codons"

JP07327677-A.
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 XX 19-DEC-1995.
 XX
 XX 07-JUN-1994; 94JP-00125125.
 XX
 XX 07-JUN-1994; 94JP-00125125.
 XX
 XX (MITK) MITSUI TOATSU CHEM INC.
 XX
 XX WPI; 1996-072335/08.
 DR P-PSDB; AAR89148.
 XX
 XX Gene(s) encoding human antibody variable regions against P.aeruginosa
 PT type B - useful for prodn. of monoclonal antibody-producing cells.
 XX
 XX Claim 4; Page 9; 12pp; Japanese.
 XX
 XX The present sequence encodes the light chain variable region of a human
 CC antibody which specifically recognises a lipopolysaccharide (LPS) antigen
 CC from Pseudomonas aeruginosa. The coding sequence can be used for
 CC preparing cell lines which produce monoclonal antibodies against the LPS.
 CC (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 333 BP; 70 A; 108 C; 77 G; 78 T; 0 U; 0 Other;
 Query Match 82.7%; Score 275.4; DB 2; Length 333;
 Best Local Similarity 89.2%; Pred. No. 2.4e-76;
 Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 CAGTCTGCCGACTGACGCTGCTGTTTAACTATGTCCTCGTACCAACAC 120
 DB 1 CAGTCTGCCGACTGACGCTGCTGTTTAACTATGTCCTCGTACCAACAC 120
 QY 61 TCCTGCACTGAAACAGGAGTGGTGGTTTAACTATGTCCTCGTACCAACAC 120
 DB 61 TCCTGCACTGAAACAGGAGTGGTGGTTTAACTATGTCCTCGTACCAACAC 120

QY 121 CACCAGCAAGCCCAAACTCATGATTATGATGTGCTAAGCGGGCTCAGGGGTC 180
 DB 121 CACCAGCAAGCCCAAACTCATGATTATGATGTGCTAAGCGGGCTCAGGGGTT 180

QY 181 TCTGATCGTCTCTGGGTCCTCAAGTCTGGCAACGCGCTCCCTGACCACTCTCGGCTC 240

DB 181 TCTACTCGCTTCTCTGGCTCCAAAGTCTGGCAACAGGCTCCCTGACCACTCTGGGCTC 240
 QY 241 CAGGCTGAGGACGAGCTGATTTACTGTTTTCATATACACGATGAGCTTGTGTTA 300
 DB 241 CAGGCTGAGGACGAGCTGATTTACTGTTTTCATATACACGATGAGCTTGTGTTA 300

RESULT 6
 ID AAZ31655
 XX AAZ31655 standard; DNA; 333 BP.
 AC AAZ31655;
 XX
 XX 13-JAN-2000 (first entry)
 DT
 XX
 XX Coding sequence for VL domain CDR of anti-estradiol antibody.
 DE
 XX Estradiol; complementarity determining region; CDR; estriol-3-sulphate;
 KW antibody antigen binding domain; steroid hormone; estriol; testosterone;
 KW dihydrotestosterone; progesterone; estriol 3-beta-di-glucuronide;
 KW menstrual cycle; hormone replacement therapy; oestrogen secreting tumour;
 KW diagnosis; VL domain; ds.
 XX
 XX Homo sapiens.
 OS
 XX US5977319-A.
 PN
 XX 02-NOV-1999.
 PD
 XX
 XX 21-OCT-1997; 97US-00958201.
 PF
 XX 21-OCT-1996; 96US-0028897P.
 PR
 XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA
 XX Johnson KS, Pope AR, Pritchard K, Williams AJ;
 PI WPI; 1999-619713/53.
 DR P-PSDB; AAV43257.
 XX
 XX New specific binding partners for estradiol, used for monitoring
 PT estradiol levels during the menstrual cycle, in hormone replacement
 PT therapy and for diagnosing estrogen secreting tumors.
 XX
 XX Disclosure; Col 27-28; 26pp; English.
 PS
 XX This sequence encodes a VL domain complementarity determining region
 CC (CDR) from an antibody specific for estradiol. The invention relates to
 CC specific binding members (sdp) comprising a polypeptide that comprises an
 CC antibody antigen binding domain (AABD) which has a dissociation constant
 CC of less than 1.0x10⁻⁸M for estradiol, and a dissociation constant of at
 CC least 500-fold higher for the steroid hormones selected from estriol,
 CC testosterone, dihydrotestosterone, progesterone, estriol-3-sulphate and
 CC estriol 3-beta-di-glucuronide, where the polypeptide comprises an
 CC antibody VH domain. The sbps can be used in an immunoassay for
 CC determining the presence or absence of estradiol in a sample. They can be
 CC used for monitoring estradiol levels, e.g. during the menstrual cycle, in
 CC hormone replacement therapy and for diagnosing oestrogen secreting
 CC tumors. The sbps can provide for discrimination between estradiol and
 CC other related steroids
 XX
 SQ Sequence 333 BP; 68 A; 101 C; 84 G; 80 T; 0 U; 0 Other;
 Query Match 82.7%; Score 275.4; DB 2; Length 333;
 Best Local Similarity 89.2%; Pred. No. 2.4e-76;
 Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 CAGTCTGCCGACTGACGCTCCCTCTGTGTCTGGTCTCTCTGGAGACGCTCACCATC 60

Db 1 CAGTCTGCTGACTGAGCCTGCTCTGTGCTGGGCTCTCTGGACAGTCGATCACCATC 60
QY 61 TCTTGCATCGAACCAGCAGATGAGCTTGGTGGTATTAACCTATGCTCTCTGGTACCAAC 120
Db 61 TCTTGCATCGAACCAGCAGATGAGCTTGGTGGTATTAACCTATGCTCTCTGGTACCAAC 120
QY 121 CACCCAGGCAAGAGCCCAAACTCATGATTTATGATGCTGAAGCGGGCTCAGGGGTC 180
Db 121 CACCCAGGCAAGAGCCCAAACTCATGATTTATGATGCTGAAGCGGGCTCAGGGGTC 180
QY 181 TCTGATCGCTTCTGCTGCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240
Db 181 CCTAATCGCTTCTGAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTC 240
QY 241 CAGCTCAGGACGAGGCTGATTTATCTGTTTATATATATATATATATATATATATAT 300
Db 241 CAGCTCAGGACGAGGCTGATTTATCTGAGCTTATCTGAGCTTATCTGAGCTTATCTG 300
QY 301 TTCGGAAGAGGAGCCCGCTTACCGCTCCTAGGT 333
Db 301 TTCGGCGGAGGAGCCCAAGCTGACCGTCTAGGT 333

RESULT 7

AAZ31654
ID AAZ31654 standard; DNA; 333 BP.

AC AAZ31654;

DT 13-JAN-2000 (first entry)

XX Coding sequence for VL domain CDR of anti-estradiol antibody.

XX Estradiol; complementarity determining region; CDR; estradiol-3-sulphate;
XX antibody antigen binding domain; steroid hormone; estradiol; testosterone;
XX dihydrotestosterone; progesterone; estradiol 3-beta-di-glucuronide;
XX menstrual cycle; hormone replacement therapy; oestrogen secreting tumour;
XX diagnosis; VL domain; ds.

XX Homo sapiens.

XX US5977319-A.

XX 02-NOV-1999.

XX 21-OCT-1997; 97US-00958201.

XX 21-OCT-1996; 96US-0028897P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Johnson KS, Pope AR, Pritchard K, Williams AJ;

XX WPI; 1999-619713/53.

XX P-PSDB; AAY43256.

XX New specific binding partners for estradiol, used for monitoring
XX estradiol levels during the menstrual cycle, in hormone replacement
XX therapy and for diagnosing estrogen secreting tumors.

XX Disclosure; Col 25-26; 26pp; English.

XX This sequence encodes a VL domain complementarity determining region
XX (CDR) from an antibody specific for estradiol. The invention relates to
XX specific binding members (abp) comprising a polypeptide that comprises an
XX antibody antigen binding domain (AABD) which has a dissociation constant
XX of less than 1.0x10⁻⁸M for estradiol, and a dissociation constant of at
XX least 500-fold higher for the steroid hormones selected from estradiol,
XX testosterone, dihydrotestosterone, progesterone, estradiol-3-sulphate and
XX estradiol 3-beta-di-glucuronide, where the polypeptide comprises an
XX antibody VH domain. The abps can be used in an immunoassay for
XX determining the presence or absence of estradiol in a sample. They can be

CC used for monitoring estradiol levels, e.g. during the menstrual cycle, in
CC hormone replacement therapy and for diagnosing oestrogen secreting
CC tumors. The abps can provide for discrimination between estradiol and
CC other related steroids

XX Sequence 333 BP; 68 A; 100 C; 84 G; 81 T; 0 U; 0 Other;

Query Match 82.2%; Score 273.8; DB 2; Length 333;

Best Local Similarity 88.9%; Pred. No. 7.6e-76;

Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 CAGTCTGCTGACTGAGCCTGCTCTGTGCTGGGCTCTCTGGACAGTCGATCACCATC 60

Db 1 CAGTCTGCTGACTGAGCCTGCTCTGTGCTGGGCTCTCTGGACAGTCGATCACCATC 60

QY 61 TCTGCTGCTGAGAACCCCAAACTCATGATTTATGATGCTGAAGCGGGCTCAGGGGTC 120

Db 61 TCTGCTGCTGAGAACCCCAAACTCATGATTTATGATGCTGAAGCGGGCTCAGGGGTC 120

QY 121 CACCCAGGCAAGAGCCCAAACTCATGATTTATGATGCTGAAGCGGGCTCAGGGGTC 180

Db 121 CACCCAGGCAAGAGCCCAAACTCATGATTTATGATGCTGAAGCGGGCTCAGGGGTC 180

QY 181 TCTGATCGCTTCTGCTGCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240

Db 181 CCTAATCGCTTCTGAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTC 240

QY 241 CAGGCTGAGGACGAGGCTGATTTATCTGTTTATATATATATATATATATATATAT 300

Db 241 CAGGCTGAGGACGAGGCTGATTTATCTGAGCTTATCTGAGCTTATCTGAGCTTATCTG 300

QY 301 TTCGGAAGAGGAGCCCGCTTACCGCTCCTAGGT 333

Db 301 TTCGGCGGAGGAGCCCAAGCTGACCGTCTAGGT 333

RESULT 8

AA503477

ID AAS03477 standard; cDNA; 330 BP.

XX AAS03477;

XX 29-AUG-2001 (first entry)

XX DNA encoding anti-adipocyte monoclonal antibody light chain, FAT 64.

XX Antibody; adipocyte; heavy chain; light chain; obesity; FAT;

XX heart disease; complementarity determining region; CDR; ss.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX P-PSDB; AAU02577.

XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.

XX Disclosure; Page 140-141; 182pp; English.

XX AAS03401-AAS03535 represent anti-adipocyte monoclonal antibody heavy and


```
XX Key Location/Qualifiers
FH misc_feature 67..108
FT /*tag= a
FT /note= "Encodes CDR 1."
FT misc_feature 154..174
FT /*tag= b
FT /note= "Encodes CDR 2."
FT misc_feature 271..294
FT /*tag= c
FT /note= "Encodes CDR 3."
FT misc_feature 307..342
FT /*tag= d
FT /note= "Framework IV. J lambda 2 segment."
XX EP581353-A1.
XX 02-FEB-1994.
XX
XX 05-JUL-1993; 93EP-00201959.
XX
XX 03-JUL-1992; 92EP-00202032.
XX
XX (NEWE-) NEDERLANDEN MIN WELZIJN.
XX
XX Osterhaus ADME;
XX
XX WPI; 1994-036603/05.
XX P-PSDB; AAR45606.
XX
XX Monoclonal antibodies to HIV-1 - directed against glycoprotein gp120,
XX useful for passive immunotherapy or prodn. of anti-idiotype vaccines.
XX
XX Claim 11; Page 17-18; 34pp; English.
XX
XX The monoclonal antibodies (MAB's) designated GP13, GP44 and GP68 react
XX with HIV-1 gp120 glycoprotein variants containing the amino acids Asn88,
XX Lys117, Asn262 and Tyr 435 but exhibit at least 50% reduced reaction with
XX gp120 variants in which these amino acids have been deleted or
XX substituted. The MAB's are useful for passive immunotherapy and their
XX anti-idiotypic antibodies can be used in the production of vaccines.
XX (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
XX correct PA field.)
XX
XX Sequence 333 BP; 69 A; 104 C; 81 G; 79 T; 0 U; 0 Other;
XX
XX Query Match 79.8%; Score 265.8; DB 2; Length 333;
XX Best Local Similarity 87.4%; Pred. No. 2.5e-73;
XX Matches 291; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
XX
XX 1 CAGTCTGCCCGAGTCAGCCCTCCCTCTGTGCTGGTCTCTGGACAGTCGGTCAACATC 60
XX |
XX 1 CAGTCTGCCCGAGTCAGCCCTCCCTCCCGCTCCGGTCTCTGGACAGTCAGTCACCATC 60
XX |
XX 61 TCCTGCACTGGAACAGCAGATGACGTTGGTGGTTATTAATACTATGTCCTCTGGTACCAAC 120
XX |
XX 61 TCCTGCTCTGGAACAGCAGTGGTGGTCTTATTAAGTATGTCCTCTGGTTCACAA 120
XX |
XX 121 CACCCGACCAAGCCCCCAACTCATGCTTATGATGCTGCTAAGCGGCTCAGGGGTC 180
XX |
XX 121 CACCCGCAAGCCCCCAACTCATGATTTATGAAGTCAATGAGCGGCTCAGGGGTC 180
XX |
XX 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
XX |
XX 181 CCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCGTCTCTGGGCTC 240
XX |
XX 241 CAGCTGAGGAGGAGGTGATATATCTGTGTTTATATACATATACACAGTACGACTTTGTTA 300
XX |
XX 241 CAACCTGAGGATGAGGCTGATTTATTTGCGCTCATATGAGGAGTAAATCATGTAATA 300
XX |
XX 301 TTCGGAAGAGGAGCCCGGTTCCACGCTCTAGGT 333
XX |
XX 301 TTCGGCGGAGGAGCAAGATTGACCGTCTAGGT 333
XX |
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```
RESULT 11
ACC85452
ID ACC85452 standard; DNA; 330 BP.
XX
XX ACC85452;
XX
XX 29-SEP-2003 (first entry)
XX
XX Human glycoprotein VI antibody IC3 variable light chain DNA.
XX
XX Human; antibody; glycoprotein VI; GPVI; 10B12; IC3; variable heavy;
XX variable light; CDR; platelet aggregation; cardiant; thrombolytic;
XX cerebroprotective; antiskling; vasotropic; cardiovascular disease;
XX Gene; ds.
XX
XX Homo sapiens.
XX
XX WO2003054020-A2.
XX
XX 03-JUL-2003.
XX
XX 18-DEC-2002; 2002WO-GB005755.
XX
XX 20-DEC-2001; 2001GB-00030543.
XX
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
XX Smethurst PA, Ouwehand WH, Farndale RW;
XX
XX WPI; 2003-559127/52.
XX
XX P-PSDB; ABR63614.
XX
XX New specific binding member binding human glycoprotein VI (GPVI) and
XX comprising an antibody VH domain and/or an antibody VL domain, useful for
XX the manufacture of a medicament for treating a disorder, e.g., thrombosis
XX or stroke.
XX
XX Disclosure; Page 88; 127pp; English.
XX
XX The present invention relates to a specific binding member which binds
XX human glycoprotein VI (GPVI), comprising an antibody VH domain and/or an
XX antibody VL domain. The antibody VH domain comprises 10B12 VH domain, IC3
XX VH domain or a VH domain comprising a VH CDR3 or optionally one or more
XX VH CDR's. The antibody VL domain comprises 10B12 VL domain, IC3 VL domain
XX and a VL domain comprising one or more VL CDRs. The specific binding
XX member is useful for the manufacture of a medicament for treating a
XX disease or disorder comprising cardiovascular conditions, thrombosis,
XX stroke, intermittent claudication, conditions with disseminated
XX intravascular coagulation, thrombocytopenic purpura, haemolytic uraemic
XX syndrome, damage to blood vessel wall resulting from surgery or therapy,
XX collagen-induced inflammation, homozygous sickle disease, kidney damage,
XX by platelet and fibrin disposition on the glomerular membrane or micro-
XX angiopathic vasculitides. The present sequence is a coding sequence of an
XX antibody domain shown in the exemplification of the invention
XX
XX Sequence 330 BP; 70 A; 100 C; 85 G; 75 T; 0 U; 0 Other;
XX
XX Query Match 78.9%; Score 262.8; DB 8; Length 330;
XX Best Local Similarity 87.3%; Pred. No. 2.2e-72;
XX Matches 288; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
XX
XX 1 CAGTCTGCCCGAGTCAGCCCTCCCTCTGTGCTGGTCTCTGGACAGTCGGTCAACATC 60
XX |
XX 1 CAGTCTGTGTTGACGAGCGCGCCCTCAATGTCCTGGCGCCCGCAGGACAGAAAGTCAACATC 60
XX |
XX 61 TCCTGCACTGGAACAGCAGATGACGTTGGTGGTTTAACTATGTCCTCTGGTACCAAC 120
XX |
XX 61 TCCTGCACTGGAACAGCAGATGACGTTGGTGGTTTAACTATGTCCTCTGGTACCAAC 120
XX |
XX 121 CACCCGAGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGCTCAGGGGTC 180
XX |
```



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XX 04-MAR-2002; 2002US-00091300.
PF
XX 10-FEB-1994; 94US-00196041.
XX 20-OCT-1994; 94US-00326552.
PR 07-JUN-1995; 95US-00476533.
PR 03-SEP-1996; 96US-00706804.
PR 07-JAN-1997; 97US-00779450.
PR 10-NOV-1997; 97US-00967113.
PR 22-SEP-1999; 99US-00401163.
PR 02-MAR-2001; 2001US-00798689.
XX (ROCK/) ROCKWELL P.
PA (GOLD/) GOLDSTEIN N I.
XX
XX Rockwell P, Goldstein NI;
PI
XX WPI; 2003-801265/75.
DR P-PSDE; ADD24422.
XX
XX Inhibiting tumor growth by administering to a human a vascular
PT endothelial growth factor receptor (VEGFR) antagonist and epidermal
PT growth factor receptor (EGFR) antagonist.
XX
XX Example 12; SEQ ID NO 28; 90pp; English.
XX
XX The invention relates to a method of inhibiting tumour growth comprising
CC administering to a human a vascular endothelial growth factor receptor
CC (VEGFR) antagonist and epidermal growth factor receptor (EGFR)
CC antagonist. The method is useful for inhibiting tumour growth. The
CC present sequence is used in the exemplification of the invention.
XX
XX Sequence 330 BP; 73 A; 104 C; 72 G; 81 T; 0 U; 0 Other;
SQ
Query Match 73.2%; Score 243.6; DB 9; Length 330;
Best Local Similarity 83.6%; Pred No. 2.4e-66;
Matches 276; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTCTGTGGTCTCCTGGACAGTGGGTACCATC 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 CAGTCTGCCCGACTCAGCCTCCCTCTGTCTGTGGTCTCCTGGACAGTGGGTACCATC 60
QY 61 TCCTGCACTGGACACCGGATGACGTGGTGGTGTATTAATATGTCTCTGGTACCAAC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 TCCTGCGCTGGAAACCAACCACTGATCTTACATATATGACCTGTCTCTGGTACCAAC 120
QY 121 CACCCAGGCAAGCCGCCAACTCATGATTTATGATGTGGCTAAGCGGCGCTCAGGGGTC 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 CACCCAGGCAAGCCGCCAACTCATGATTTATGATGTGGCTAAGCGGCGCTCAGGGGTC 180
QY 181 TCTGATGCTTCTCTGGCTCCAGCTGGACACACCGGCTCCCTGACCATCTCTGGGCTC 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TCTAATGGCTTCTCTGGCTCCAGCTGGACACACCGGCTCCCTGACCAATCTCTGGACTC 240
QY 241 CAGGCTGAGGACGAGGCTGATTACTGTGTTCATATACCAACAGTAGCACTTTGTTA 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 CAGGCTGAGGACGAGGCTGATTACTGTGTTCATATACCAACAGTAGCACTTTGTTA 300
QY 301 TTCGGAAGGAGGACCGGTTGACCGTCCTA 330
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 TTCGGAACCTGGGACCAAGGTCACCGTCCTA 330

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Search completed: June 19, 2004, 03:30:41
Job time : 279 secs

[illegible]

RESULT 2

US-08-958-201-11
Sequence 11, Application US/08958201
Patent No. 5977319
GENERAL INFORMATION:
APPLICANT: Pope, Anthony R
APPLICANT: Pritchard, Kevin
APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific binding members for estradiol;
TITLE OF INVENTION: materials and methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPC)
CURRENT APPLICATION DATA: 201
APPLICATION NUMBER: US/08/958,201
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-OCT-1996
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: D12 (light chain)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..333
US-08-958-201-11

```

Query Match      82.2%; Score 273.8; DB 2; Length 333;
Best Local Similarity 88.9%; Pred. No. 2e-77;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 CAGTCTCCCGACTCAGCCTCCCTCTGTCTGTGGGTCTCTGGACAGTCGGTCACCATC 60
Db 1 CAGTCTCTGTACTCAGCCTGCCTGTGTGTGTGGTCTCTCTGGACAGTCGGTCACCATC 60

```

Query Match	57.7%;	Score 192;	DB 2;	Length 333;
Best Local Similarity	77.4%;	Pred. No. 1.7e-51;		
Matches 260;	Conservative 0;	Mismatches 70;	Indels 6;	Gaps 2;
QY	1	CAGTCTGCCCGCCAGCTCAGGCTCCCTCTGTCTGTGGGTCTCTCGGACAGTGGTACCAATC	60	
DB	1			
QY	61	TCTGTCAGCTGGAAACAGGATGACGTGGTGGTATTAACTATCTCTCTGGTACCAACAC	120	
DB	61			
QY	121	CACCCAGGCAAGCCCCCAACTCATGATTTATGATGTGCGTTAAGGGGGCTCAGGGGCTC	180	
DB	118	CACCAGGCAAGCCCCCAACTCATGATTTATGATGTGAGTAAAGGGGGCTCAGGGGCTC	177	
QY	181	TCTGATCGTTCTCTGGCTCCAGTCTGGCAGACACAGGCGCTCCCTGACCACTCTCTGGGCTC	240	
DB	178	CTTGACCGGATTTCTTGGCTCCAGTCTGGCACTCGACCTCCCTTGGACATCAGTGGGCTC	237	
QY	241	CAGGCTGAGGAGGAGGCTGATTATTACTGTGTGTTTCAT---ATACAAACAGTAGCACTTTG	297	
DB	238	CAGTCTGAGATGAGGCTGATTATTACTGTGCGAGCATGGATGACAGCTGTGAGTGAATTT	297	
QY	298	TTATTTCGGAAGGGAGACCCGGTTGACCGTCTTAGGT	333	
DB	298	CTCTTCGGAACCTGGGACCAAGCTGGAGATCAAACTG	333	

```

RESULT 6
US-09-240-274-132
; Sequence 132, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 001
US-09-240-274-132

Query Match          53.6%; Score 178.6; DB 3; Length 330;
Best Local Similarity 74.5%; Pred. No. 3.1e-47;
Matches 239; Conservative 0; Mismatches 79; Indels 3; Gaps 1;

QY 13 ACTCAGCCTCCCTCTGTGTCTGGGTCTCTCTGGGACAGTGGGTCAACATCTCTGTGCACTGGA 72
DB 10 ACCGAGCGCCCTCAGTGTCTGGGGCCCGAGGGCAGAGGGTCAACATCTCTGTGCACTGGG 69
QY 73 ACCAGCGATCAGGTTGGTGGTTATTAATATGTCTCTCTGGTACCAACACACCACCGAGGAAA 132
DB 70 AGCAGCTCCAACTCGGGGACCCCTTATGSGTGTACACTGGTACCAAGAGTTTCCAGGAACA 129
QY 133 GCCCCCAAACCTCAATTTATGATGTCGCTAAAGGGGGCCCTCAGGGGTCTCTGATCGGCTTC 192
DB 130 GCCCCCAAACCTCGTCATCTCAATATGACAAATCGGCCCTCAGGGGTCCCTGACCGATTC 189
QY 193 TCTGGGTCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGTGGCTTCCAGGGTTCAGGAC 252
DB 190 TCTGGGTCCAAGTCTGGCACTCCCTCAGCCCTCCCTGGCCATCACTGGGCTCCAGGGCTGAGGAT 249
QY 253 GAGGCTGATTTACTGTTGTTTCATATACAAACGAG---TAGCACTTTTGTATTTCGGAAGA 309
DB 250 GAGGCTGATTTACTGTCGCACTCTATGACAGCCCTGATGGAAGGGTGTTCGGCGGA 309
QY 310 GGGACCGGGTTGACCGGTCCTTA 330
DB 310 GGGACCAAGCTGACCGGTCCTTA 330

```

RESULT 7
US-08-199-911-1
; Sequence 1, Application US/08199911
; Patent No. 5495002
; GENERAL INFORMATION:
; APPLICANT: Kobrin, Barry J.
; APPLICANT: Haspel, Martin V.
; TITLE OF INVENTION: Tumor Associated Monoclonal Antibody
; TITLE OF INVENTION: 123AV16
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AKZO NOBEL
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,911
FILING DATE: 22-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,517
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/636,179
FILING DATE: 31-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/302,155
FILING DATE: 25-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/697,078
FILING DATE: 31-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/575,533
FILING DATE: 31-JAN-1984
ATTORNEY/AGENT INFORMATION:
NAME: Goimley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-258-5200
TELEFAX: 301-977-0847
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: B-lymphocyte
CELL LINE: 123AV16
IMMEDIATE SOURCE:
CLONE: 123AV16-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..330
FEATURE:
NAME/KEY: misc_binding
LOCATION: 67..106
FEATURE:
NAME/KEY: misc_binding
LOCATION: 152..173
FEATURE:
NAME/KEY: misc_binding
LOCATION: 270..303
US-08-199-911-1

```

	Query Match	52.9%;	Score 176.2;	DB 1;	Length 330;
	Best Local Similarity	74.8%;	Pred. No. 1.8e-46;		
	Matches 249;	Conservative 0;	Mismatches 78;	Indels 6;	Gaps 2;
Qy	1	CAGTCTGCCCGACTCAGCCTCCCTCTGTCTGTGGGTCTCTGGACAGCTGGGTCAACATC	60		
Db	1	CAGTCTGCTTGAAGCAGCGCCCTCAGTATCTGGCGCCCGACAGACAGAAGGTCAACATC	60		
Qy	61	TCTTGCACCTGGAAACAGAGCATGACGTTGGTGGTTATACTATGTCTCTGGTACCAACAC	120		
Db	61	TCTTGTCTCTGGAAACAGCTCCAACT---TGGGAATAATTTTGTATCTCTGGTACCAACAA	117		
Qy	121	CACCCAGGCAAGGCCCCCAACTCATGATTATGATGCGCTAAGCGGGCCCTCAGGGGTC	180		

US-08-264-093-5
; Sequence 5, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adeleide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R. 31081
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-264-093-5

Query Match 50.5%; Score 168; DB 1; Length 333;
Best Local Similarity 72.9%; Pred. No. 7.1e-44;
Matches 245; Conservative 0; Mismatches 85; Indels 6; Gaps 2;

QY 1 CAGTCTGCCCCGACTCAGCCCTCCTGTGTCTGGGTCTCTCTGGACAGTGGTCCACCATC 60
DB 1 CAGTCTGTGTGACTCAGCCACCTCAGCGTCTGGGACCCCGGCGAGAGGGTCCACCATC 60

QY 61 TCCTGCATGAACACGAGGATGAGTGGTGGTTATTAATCTCTCTGTATCCACAC 120
DB 61 TCTTGTCTGGAGCAGCTCCACATCGGAACCTAATA---CTGTAACCTGGTACCTGCAG 117

QY 121 CACCCAGGCAAGCCCCAACTCATGATTTATGATGCTGAAGCGGGCTTCAGGGGTC 180
DB 118 CTCCAGGAGCGCCCCCAAGTCTCATCTATAGTAATAATCAGCGGCCCTCAGGGGTC 177

QY 181 TCTGATCGCTTCTCTGGCTCAGTCTGGCAACAGCGCTCCCTGACATCTCTGGGCTC 240
DB 178 CTTGACCGATTTCTGGCTCCAGTCTGGCACTCAGCCCTCCCTGGCCATCAGTGGACT 237

QY 241 CAGCTGAGGACGAGGCTGATTTACTTGTGTTTCAT---ATACAACAGTAGCACTTTG 297
DB 238 CAGTCTGAGGATGAGGCTGATTTCTGTGCAGCATGGGATGACAGCTGAAAGGTGTG 297

QY 298 TTATTCGGAAGAGGAGCCCGGTTGACCGTCTCTAGGT 333
DB 298 GTATTGCGGAGGAGGACCAAGCTGACCGTCTCTAGGT 333

RESULT 11
US-09-240-274-126

; Sequence 126, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain L05
US-09-240-274-126

Query Match 49.3%; Score 164.2; DB 3; Length 327;
Best Local Similarity 73.8%; Pred. No. 1.1e-42;
Matches 237; Conservative 0; Mismatches 78; Indels 6; Gaps 2;

QY 13 ACTCAGCCCTCCTCTGTGTCTGGGTCTCTCTGGACAGTGGTCCACCATCTCTCTGCACTGGA 72
DB 10 ACTCAGCCACCTCCTCAGCGTCTGGGACTCCCGGGCTGAGGGTCAACCATCTCTTGTCTGGA 69

QY 73 ACCAGGATGAGCTTGGTGGTTATTAATCTCTCTGTGTACCAACACACCCAGGCAAA 132
DB 70 AGCAGCTCCACATCGGAAGTAATA---TTGTAACCTGGTACCAAGCTCCCGGATTC 126

QY 133 GCCCCCAACTCATGATTTATGATGCTGAAGCGGGCTTCAGGGGTCTCTGATCGCTTC 192
DB 127 GCCCCCAACTCTCATCTTTAGTAATAATAGCGGCCCTCAGGGGTCTCTGACCGATTC 186

QY 193 TCTGGCTCAAGTCTGGCAACACCGGCTCCCTGACATCTCTGGGCTCCAGGCTGAGGAC 252
DB 187 TCTGGCTCAAGTCTGGCAACCTCAGCCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGAT 246

QY 253 GAGGCTGATTATTACTTGTGTTTCAT---ATACAACAGTAGCACTTTGTTATTTCGGAAGA 309
DB 247 GAGGCTGATTATTACTTGTGTTTCATGATGATGATGATGATGATGATGATGATGATGAT 306

QY 310 GGGACCGGTTGACCGTCTTA 330
DB 307 GGGACCAAGCTGACCGTCTTA 327

RESULT 12
US-09-240-274-223
; Sequence 223, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 223
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 130
LENGTH: 327
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain N01
US-09-240-274-130

Query Match 48.3%; Score 161; DB 3; Length 327;
Best Local Similarity 73.2%; Pred. No. 1.2e-41;
Matches 235; Conservative 0; Mismatches 80; Indels 6; Gaps 2;
Qy 13 ACTCAGCCTCCCTCTGTCCTGGTCTCTGGACAGTCGGTCACCATCTCTGCACTGGA 72
Db 10 ACGCAGCGCCCTCAGTGTCTGGCGCCCGCAGGACAGAGTCACCATCTCTGCTCTGGA 69
Qy 73 ACCAGCGATGACGTTGCTGTATTAATATGTCCTCTGGTACCAACACCCAGGCAGA 132
Db 70 AGCAGCTCCACATGTACG---TAACTATGTCCTGGTACCCAGCAGCTCCAGGAACA 126
Qy 133 GCCCCCAAACTCATGATTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCTGATCGCTTC 192
Db 127 GCCCCCAAACTCCTCATTTTGACATTTATAGGCGACCCCTCAGGGATTCCTGACCGATT 186
Qy 193 TCTGGCTCCAACTCTGGCAACACAGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGAC 252
Db 187 TCAGGCTCCAACTCTGGCACTGAGCCACCTGGGCACTCCAGACTCCAGACTGGGAC 246
Qy 253 GAGGCTGATTATTAATCTGTTGTCAT---ATACACCAAGTAGCATTGTTATTTCGGAAGA 309
Db 247 GAGGCCGATTATTACTGTGCAACATGGGATGACAGCCCTGAATGGTGGGTGTTGGCGGA 306
Qy 310 GGGACCGGTTGACCGTCCTA 330
Db 307 GGGACCAAGCTGACCGTCCTA 327

Search completed: June 19, 2004, 04:31:43
Job time : 64 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 03:26:07 ; Search time 284 Seconds
(without alignments)
5371.489 Million cell updates/sec

Title: US-09-019-441a-1_COPY_58_390

Perfect score: 333

Sequence: 1 cagctgccccgactgagcc.....ccgggttgacgctcctaggt 333

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 2527274

Minimum DB seq length: 0

Maximum DB seq length: 333

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284.6	85.5	331	13	US-10-342-887-200
2	284.6	85.5	331	13	US-10-172-118-200
3	275.8	82.8	330	17	US-10-399-518-96
4	271.8	81.4	319	17	US-10-663-244-86
5	245.2	73.6	294	15	US-10-029-386-14141
6	243.6	73.2	330	15	US-10-091-300-28
7	242	72.7	330	15	US-10-091-300-38
8	239.6	72.0	324	10	US-09-848-798-137
9	239.2	71.8	300	9	US-09-879-813-85
10	239.2	71.8	300	15	US-10-146-505-85
11	237	71.2	294	9	US-09-864-761-27886
12	219.6	65.9	278	15	US-10-029-386-15224
13	218.4	65.6	246	13	US-09-734-613-15
14	214.8	64.5	243	13	US-09-734-613-16

15	210.4	63.2	246	13	US-09-734-613-21	Sequence 21, Appl
16	208.8	62.7	312	10	US-09-848-798-138	Sequence 138, App
17	202	60.7	330	13	US-10-371-942-11	Sequence 11, Appl
18	198.4	59.6	241	13	US-09-734-613-22	Sequence 22, Appl
C 19	189.6	56.9	248	9	US-09-864-761-27886	Sequence 27886, A
20	187.4	56.3	333	15	US-10-199-908-3	Sequence 3, Appli
C 21	186.2	55.9	309	10	US-09-918-995-18427	Sequence 18427, A
C 22	184.6	55.4	309	10	US-09-918-995-18429	Sequence 18429, A
23	184.2	55.3	333	15	US-10-091-300-40	Sequence 40, Appl
24	179.6	53.9	322	13	US-10-342-887-1926	Sequence 1926, Ap
25	179.6	53.9	322	13	US-10-172-118-1926	Sequence 1926, Ap
26	178.8	53.6	330	10	US-09-848-798-132	Sequence 132, App
27	177.8	53.4	333	15	US-10-091-300-46	Sequence 46, Appl
28	176.8	53.1	333	15	US-10-091-300-34	Sequence 34, Appl
29	176.8	53.1	333	15	US-10-091-300-50	Sequence 50, Appl
30	171.4	51.5	330	17	US-10-440-522-3	Sequence 3, Appli
31	170.4	51.2	333	15	US-10-091-300-48	Sequence 48, Appl
32	169	50.8	330	10	US-09-848-798-134	Sequence 134, App
33	168.2	50.5	330	17	US-10-440-522-2	Sequence 2, Appli
34	164.2	49.3	327	10	US-09-848-798-126	Sequence 126, App
35	164.2	49.3	327	10	US-09-848-798-223	Sequence 223, App
36	162.6	48.8	327	10	US-09-848-798-129	Sequence 129, App
37	162.6	48.8	333	15	US-10-091-300-21	Sequence 21, Appl
38	161	48.3	327	10	US-09-848-798-138	Sequence 138, App
39	161	48.3	327	10	US-09-848-798-130	Sequence 130, App
40	155.4	46.7	330	13	US-10-371-942-43	Sequence 43, Appl
41	153.6	46.1	327	10	US-09-848-798-124	Sequence 124, App
42	153	45.9	327	10	US-09-848-798-123	Sequence 123, App
43	153	45.9	327	10	US-09-848-798-125	Sequence 125, App
44	145	43.5	234	15	US-10-153-437-3	Sequence 3, Appli
45	140.2	42.1	327	10	US-09-848-798-127	Sequence 127, App

ALIGNMENTS

RESULT 1

US-10-342-887-200
; Sequence 200, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 200
; LENGTH: 331
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-200

Query Match 85.5%; Score 284.6; DB 13; Length 331;

Best Local Similarity 91.2%; Pred. No. 4.4e-87;

Matches 302; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 CAGCTGCCCGACCTCAGCTCCCTCTGTCTGGCTCTCCCTGGACAGTGGCTCACCATC 60

Db 1 CAGCTGCCCGACCTCAGCTCCCTCTGTCTGGCTCTCCCTGGACAGTGGCTCACCATC 60

Qy	61	TCTCGAC	TGGAAAC	CAGCGAT	TGACG	TGTTGG	TGGTTAT	AAC	TATG	TCTCTG	TGTTCC	AGAC	120	
Db	61	TCTCGAC	TGGAAAC	CAGCAG	TGACG	TGTTGG	TGGTTAT	AAC	CA	TG	TCTCTG	TGTTCC	AGCA	120
Qy	121	CACCCAG	GAACG	CCCAACT	CATG	ATTTAT	GATG	TC	GCTA	AGCG	GGCTC	CAGGG	180	
Db	121	CACCCAG	GAACG	CCCAACT	CATG	ATTTAT	GGTG	CA	TA	TGGCC	CTCAG	GGGT	180	
Qy	181	TCTGAT	CGCTT	CTCTGG	CTCC	AAGTCT	GGCAAC	CAC	GGCTCC	CTTG	ACATCT	CTGGG	240	
Db	181	TCTAAT	CGCTT	CTCTGG	CTCC	AAGTCT	GGCAAC	CAC	GGCTCC	CTTG	ACATCT	CTGGG	240	
Qy	241	CAGGCT	GAGGA	CAGGCT	GATTAT	TACTGT	TGTTCA	TAT	ACAC	CAGTAG	CACTTT	GGTA	300	
Db	241	CAGGCT	GAGGA	CAGGCT	GATTAT	TACTGT	CA	GTCT	AT	ACAG	CGAG	CACT	300	
Qy	301	TTCGA	AGAGG	ACCGG	TTG	CAC	CTC	TAG					331	
Db	301	TTCGG	CGAGG	ACCAAG	CTC	AC	CTC	TAG					331	

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RESULT 2
US-10-172-118-200
  ; Sequence 200, Application US/10172118
  ; Publication No. US20030224374A1
  ; GENERAL INFORMATION:
  ; APPLICANT: Dai, Hongyue
  ; APPLICANT: He, Yudong
  ; APPLICANT: Linsley, Peter
  ; APPLICANT: Mao, Mao
  ; APPLICANT: Roberts, Chris
  ; APPLICANT: Van 't Veer, Laura
  ; APPLICANT: Van de Vijver, Marc
  ; APPLICANT: Bernards, Rene
  ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
  ; FILE REFERENCE: 9301-175-999
  ; CURRENT APPLICATION NUMBER: US/10/172.118
  ; CURRENT FILING DATE: 2002-06-14
  ; PRIOR APPLICATION NUMBER: 60/380,770
  ; PRIOR FILING DATE: 2002-05-14
  ; NUMBER OF SEQ ID NOS: 2699
  ; SEQ ID NO 200
  ; LENGTH: 331
  ; TYPE: DNA
  ; ORGANISM: Homo sapiens
  ; PUBLICATION INFORMATION:
  ; DATABASE ACCESSION NUMBER: AJ249377
  ; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-200

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Query Match	85.5%	Score 284.6	DB 13	Length 331
Best Local Similarity	91.2%	Pred. No. 4.4e-87		
Matches 302	Conservative 0	Mismatches 29	Indels 0	Gaps 0
Qy	1	CAGTCTGCCCGCAGCTCAGCTCCCTCTCTGTCCTCGGTCTCTCTGACAGTGGTCAACATC	60	
Db	1	CAGTCTGCCCTGACTCAGCTCGCTCTCGGTCTCTCTGACAGTGGTCAACATC	60	
Qy	61	TCCTGCACTGGAAACAGCGAGTGAAGTTGGTGGTTATAACTATGTCTCTCTGGTACCAACAC	120	
Db	61	TCCTGCACTGGAAACAGCGAGTGAAGTTGGTGGTTATAAACCATGTCTCTCTGGTACCAACAA	120	
Qy	121	CACCAGGCAAAAGCCCCCAACTCATGATTTATGATGTGGTACAGGGGCTCTAGGGGCTC	180	
Db	121	CACCAGGCAAAAGCCCCCAACTCATGATTTATGGTGTCAAGTAATCGCCCCCTCAGGGGGTT	180	
Qy	181	TCTGATCGCTTCTCTGGCTCCAGTCTGGCAACACGGGCTCCCTCGACCATCTCTGGGCTC	240	
Db	181	TCTAATCGCTTCTCTGGCTCCAGTCTGGCAACACGGGCTCCCTCGACCATCTCTGGGCTC	240	
Qy	241	CAGGCTCAGGACGAGGGCTGATTTACTGTGTTTCATATACAAACAGTAGCACTTTGTTA	300	

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Db      241  CAGCGTCAGAGCGGCTGATTATCTACGACGTCATATATCAGACGACGACACTCGGCTG 330
Qy      301  TTCGAAAGAGGAGCCCGGTTGACCGTCCTAG 331
Db      301  TTCGCGAGGAGGACCAAGCTGACCGTCCTAG 331

RESULT 3
US-10-399-518-96
; Sequence 96, Application US/10399518
; Publication No. US20040091475A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: YABUTA, NAOHIRO
; APPLICANT: TSUNODA, HIROYUKI
; APPLICANT: ORITA, TETSURO
; TITLE OF INVENTION: DEGRADED TPO AGONIST ANTIBODY
; FILE REFERENCE: 065678/0111
; CURRENT APPLICATION NUMBER: US/10/399,518
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: PCT/JF01/03288
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: JP 2001-277314
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: JP 2000-321821
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 96
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Mus sp.
US-10-399-518-96

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Query Match	82.8%;	Score 275.8;	DB 17;	Length 330;
Best Local Similarity	90.2%;	Pred. No. 4,6e-84;		
Matches 295;	Conservative 0;	Mismatches 32;	Indels 0;	Gaps 0;
Qy	4	TCCTGCCCGGACTCAGCCTCCCTCGTGTCTCGGGTCTCTCTGGACAGTCGGTCACCATCTCC	63	
Db	4	TATGTGTGACTCAGCCACCCCTCGTGTCTAGGGTCTCTGGACAGTCGATCACCATCTCC	63	
Qy	64	TGCACCTGGAACACGACGATGACGTTGGTGGTTATAACTATGTCTCTCGGTACCAACACAC	123	
Db	64	TGCACCTGGAACACGACGATGAGGTTGGTGGTTATACTATGTCTCTCGGTACCAACAGCAC	123	
Qy	124	CCAGGCAAAAGCCCCCAAACTCATGATTTATGATGTCTGCTAAGCGGGCTCTCAGGGGTCTCT	183	
Db	124	CCAGGCAAAAGCCCCCAAACTCATGATTTATGAGGGCAGTAAACGGCCCTCAGGGGGTTCT	183	
Qy	184	GATGCTTCTCTCGCTCCAGTCTGGCAACACGGCCCTCCTGACCATCTCTGGGCTCCAG	243	
Db	184	AATGCTTCTCTCGCTCCAGTCTGGCAACACGGCCCTCCTGACCATCTCTGGGCTCCAG	243	
Qy	244	GCTGAGGACGAGGCTGATTATTACTGTGTTCATATACAACCAAGTAGCATTGTTATTTC	303	
Db	244	GCTGAGGACGAGGCTGATTATTACTGAGCTCATATACAACCAAGTAGCATTGTTATTTC	303	
Qy	304	GGAAGAGGACCCGGTTGACCGTCTTA	330	
Db	304	GGCGGAGGACCAAGCTGACCGTCTTA	330	

RESULT 4
US-10-663-244-86
: Sequence 86, Application US/10663244
: Publication No. US20040110933A1
: GENERAL INFORMATION:
: APPLICANT: London, Isaac J.
: APPLICANT: Edge, Albert
: APPLICANT: Kent, Rachel Baribault
: TITLE OF INVENTION: CD44 LIGANDS

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/ FILE REFERENCE: 10280-063001
/ CURRENT APPLICATION NUMBER: US/10/663,244
/ CURRENT FILING DATE: 2003-09-15
/ PRIOR APPLICATION NUMBER: US 60/410,758
/ PRIOR FILING DATE: 2002-09-13
/ PRIOR APPLICATION NUMBER: US 60/469,123
/ PRIOR FILING DATE: 2003-05-09
/ NUMBER OF SEQ ID NOS: 165
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 86
/ LENGTH: 319
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetically generated oligonucleotide
US-10-663-244-86

Query Match      81.4%; Score 271; DB 17; Length 319;
Best Local Similarity 90.6%; Pred. No. 2e-B2;
Matches 289; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 12 GACTCAGCCTCCCTCTGCTGGTCTCCCTGGACAGTCGCTACCAATCTCTGACATGG 71
Db 1 GACTCAGCCTCCCTCCGCTGCTGGTCTCCCTGGACAGTCGATCAACATCTCTGCACTGG 60

Qy 72 AACACGCGATCAGCTGGTGGTTAATCTATGTTCTCTGGTACCAACACACCCAGGCAA 131
Db 61 AACACGAGTACGCTGGTGGTTAATCTATGTTCTCTGGTACCAACACACCCAGGCAA 120

Qy 132 AGCCCCAACTCATGATTTATGATGTCGCTAAGCGGCCCTCAGGGGTCTCTGATCGCTT 191
Db 121 AGCCCCAACTCATGATTTATGATGTCAGTAATCGGCCCTCTGGGGTTTCTATATCGCTT 180

Qy 192 CTCTGGCTCCAGTCTGCAACAGCGCTCTCTGACCATCTCTGGCTCCAGGCTGAGGA 251
Db 181 CTCTGGCTCCAGTCTGCAACAGCGCTCTCTGACCATCTCTGGCTCCAGGCTGAGGA 240

Qy 252 CGAGGCTGATTAATCTCTGCTCATATACACAGTAGCACTTTGTTATTCGGAAGAGG 311
Db 241 CGAGGCTGATTAATCTCTGCTCATATACAGTAGCACTTTGTTATTCGGAAGAGG 300

Qy 312 GACCGGTTGACCGTCTTA 330
Db 301 GACCGGTTGACCGTCTTA 319
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RESULT 5

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US-10-029-386-14141/c
/ Sequence 14141, Application US/10029386
/ Publication No. US20030194704A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David K.
/ APPLICANT: Hanzel, David K.
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
/ TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
/ FILE REFERENCE: AEWICA-X-2
/ CURRENT APPLICATION NUMBER: US/10/029,386
/ CURRENT FILING DATE: 2001-12-20
/ NUMBER OF SEQ ID NOS: 34288
/ SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 14141
/ LENGTH: 294
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO CHR22 155.0
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.52
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.6
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.53
/ OTHER INFORMATION: NT HIT: Z85032.1, EVALUE 0.00e+00
/ OTHER INFORMATION: SWISSPROT HIT: P01705, EVALUE 3.00e-47
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/ OTHER INFORMATION: EST_HUMAN HIT: BG754419.1, EVALUE 0.00e+00
US-10-029-386-14141

Query Match      73.6%; Score 245.2; DB 15; Length 294;
Best Local Similarity 91.8%; Pred. No. 1.4e-73;
Matches 259; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGCTCTGGGTCTCTCTGGACAGTCGGTCAACATC 60
Db 283 CAGTCTGCCCGGACTCAGCCTCCCTCTGCTCTGGGTCTCTCTGGACAGTCGATCAACATC 224

Qy 61 TCCTGCACTGGAAACGAGCGATGAGTGTGGTGGTTAACTATGTTCTCTGGTACCAACAC 120
Db 223 TCCTGCACTGGAAACGAGCGATGAGTGTGGTGGTTAACTATGTTCTCTGGTACCAACAG 164

Qy 121 CACCCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTC 180
Db 163 CACCCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTC 104

Qy 181 TCCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACAGGCTTCCCTGACCATCTCTGGGCTC 240
Db 103 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACAGGCTTCCCTGACCAATCTCTGGGCTC 44

Qy 241 CAGGCTGAGGACGAGCTGATTAATTAATGTTTCTATATACA 282
Db 43 CAGGCTGAGGACGAGCTGATTAATTAATGTTTCTATATACA 2

RESULT 6
US-10-091-300-28
/ Sequence 28, Application US/10091300
/ Publication No. US20030108545A1
/ GENERAL INFORMATION:
/ APPLICANT: Rockwell, Patricia
/ APPLICANT: Goldstein, Neil I.
/ TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
/ TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
/ FILE REFERENCE: 11245/46211
/ CURRENT APPLICATION NUMBER: US/10/091,300
/ CURRENT FILING DATE: 2002-03-04
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 28
/ LENGTH: 330
/ TYPE: DNA
/ ORGANISM: Human
US-10-091-300-28

Query Match      73.2%; Score 243.6; DB 15; Length 330;
Best Local Similarity 83.6%; Pred. No. 5.1e-73;
Matches 276; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGCTCTGGGTCTCTCTGGACAGTCGGTCAACATC 60
Db 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGCTCTGGGTCTCTCTGGACAGTCGATCAACATC 60

Qy 61 TCCTGCACTGGAAACGAGCGATGAGTGTGGTGGTTAACTATGTTCTCTGGTACCAACAC 120
Db 61 TCCTGCACTGGAAACGAGCGATGAGTGTGGTGGTTAACTATGTTCTCTGGTACCAACAG 120

Qy 121 CACCCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTC 180
Db 121 CACCCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTC 180

Qy 181 TCCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACAGGCTTCCCTGACCATCTCTGGGCTC 240
Db 181 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACAGGCTTCCCTGACCAATCTCTGGGCTC 240

Qy 241 CAGGCTGAGGACGAGCTGATTAATTAATGTTTCTATATACAACAGTAGCAGCTTTGTTA 300
Db 241 CAGGCTGAGGACGAGCTGATTAATTAATGTTTCTATATACAACAGTAGCAGCTTTGTTA 300

Qy 301 TTCGGAAGAGGACCGCGTGGACCGTCTTA 330
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rn(D) chain R01
US-09-848-798-137

Query Match 72.0%; Score 239.6; DB 10; Length 324;
Best Local Similarity 86.8%; Pred. No. 1.2e-71;
Matches 276; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

Qy 13 ACTGAGCTCCTCTGTGTCTCTGGGTCTCTGTGACAGTCGGTCACCATCTCCTGCACCTGGA 72
Db 10 ACTGAGCTCCTCTCGCGCTCCGGGTCTCTGTGACAGTCAGTCACCATCTCCTGCACCTGGA 69

Qy 73 ACCAGCGATGAGCTTGGTGGTTTATAACTATGTCTCTGTGTACCAACACCAACCCAGGCAA 132
Db 70 GCCAGCAGTGACGTGGTGCTTTATAAGCAGCTCTCTGGTACCAACACCAACCCAGGCAA 129

Qy 133 GCCCCAACTCATGTTATGATGTGCTGTAGCGGCTCTCAGGGCTCTGTGATCGCTTC 192
Db 130 GCCCCAAACTCCTGACTCATGAGGCACTAAGCGGCTCTCTGGGCTCTCAGGGCTGAGGAT 189

Qy 193 TCTGGCTCCAACTCTGGCAACACGGCTCCCTGACCATCTCTGGGTCCAGGCTGAGGAC 252
Db 190 TCTGGCTCCAACTCTGGCAACACGGCTCCCTGACCGTCTCTGGGCTCTCAGGGCTGAGGAT 249

Qy 253 GAGGCTGATTATGCTGTGTTTCATATACACCGATGACACATTTGTTATTCGGAAGAGGG 312
Db 250 GAGGCTGATTATGCTGAGCTCATTTGCA---GGTAATTCGTGTATATTCGCGGAGGG 306

Qy 313 ACCCGGTTGACCGTCTTA 330
Db 307 ACCAAGCTGACCGTCTTA 324

RESULT 9
US-09-879-813-85
; Sequence 85, Application US/09879813
; Patent No. US20020155453A1
; GENERAL INFORMATION:
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OP INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005
; CURRENT APPLICATION NUMBER: US/09/879,813
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-879-813-85

Query Match 71.8%; Score 239.2; DB 9; Length 300;
Best Local Similarity 89.7%; Pred. No. 1.6e-71;
Matches 269; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

Qy 19 CCTCCTCTGTGTCTGGGTCTCTGTGACAGTCGGTCACCATCTCCTGCACCTGGAACGAGC 78
Db 1 CCTGCTCGTGCTCTGGGTCTCTGTGACAGTCGATCACCATCTCTCTGCACTGGAACGAGC 60

Qy 79 GATGAGCTTGGGTGTATATGATCTCTCTGGTACCAACACCAACCCAGGCAAGCCCC 138
Db 61 AGTGAGCTTGGGTGTATATGATCTCTCTGGTACCAACAAACCCAGGCAAGCCCC 120

Qy 139 AAATCATGATTTATGATGTCTGCTAAGCGGGCTCTCAGGGCTCTCTGATCGTTCTCTGCG 198
Db 121 AAATCATGATTTATGATGTCTGATGATGCGGCTCTCAGGATTTCTAATCGTTCTCTGCG 180

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QY 199 TCCAACTGCGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGCAAGAGCT 258
DB 181 TCCAACTGCGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGCAAGAGCT 240
QY 259 GATTATTACTGTTGTTTATATACCAACAGTACCA---CTTTGTTATTTCGAGAGAGGAGCC 315
DB 241 GATTATTACTGTTGTTTATATACCAACAGTACCA---CTTTGTTATTTCGAGAGAGGAGCC 300

RESULT 10

US-10-146-505-85
; Sequence 85, Application US/10146505
; Publication No. US20030108889A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: GB 9901141.3
; PRIOR FILING DATE: 1998-01-19
; PRIOR APPLICATION NUMBER: GB 9913435.5
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-505-85

Query Match 71.8%; Score 239.2; DB 15; Length 300;
Best Local Similarity 89.7%; Pred No. 1.6e-71;
Matches 269; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

QY 19 CTTCCCTCTGTTCTGGGCTCTCTGACAGTCGGTCAACATCTCTGCACTGGAACGAGC 78
DB 1 CTTGCTCTGTTCTGGGCTCTCTGACAGTCGATCACCATCTCTGCACTGGAACGAGC 60
QY 79 GATGACCTGGTGGTTATATATCTCTCTGTTACCAACACCCAGGCAAGGAGCC 138
DB 61 AGTGACCTGGTGGTTATATATCTCTCTGTTACCAACACCCAGGCAAGGAGCC 120
QY 139 AAACATCATGATTATGATGTCGCTAAGCGGGCTCAGGGGCTCTGTGATCGCTTCTCTGGC 198
DB 121 AAACATCATGATTATGATGTCAGTAATCGGCCCTCAGGGATTTCTAATCGCTTCTCTGGC 180
QY 199 TCCAACTGCGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGCAAGAGCT 258
DB 181 TCCAACTGCGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGCAAGAGCT 240
QY 259 GATTATTACTGTTGTTTATATACCAACAGTACCA---CTTTGTTATTTCGAGAGAGGAGCC 315
DB 241 GATTATTACTGTTGTTTATATACCAACAGTACCA---CTTTGTTATTTCGAGAGAGGAGCC 300

RESULT 11

US-09-864-761-22661
; Sequence 22661, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 22661
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002308.1
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: NT HIT: X14616.1, EVALUATE 0.00e+00
; OTHER INFORMATION: EST HUMAN HIT: A406348.1, EVALUATE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P01705, EVALUATE 4.00e-45
US-09-864-761-22661

Query Match 71.2%; Score 237; DB 9; Length 294;
Best Local Similarity 91.0%; Pred No. 8.9e-71;
Matches 252; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 20 CTCCTCTGTTCTGGGCTCTCTGAGAGTCGGTCCACATCTCTGCACTGGAACGAGCG 79
DB 1 CTGCTCCGTTCTGGGCTCTCTGAGAGTCGATCACCATCTCTGCACTGGAACGAGCA 60
QY 80 ATGACGTTGGTGGTTATATCTCTCTGTTACCAACACCCAGGCAAGGAGCC 139

D _b	61	GTGATGTTGGGAGTTATTAACCTGTGCTCTCGGTACCAACAGCACCCAGGCAAGGCCCCCA	120
Q _y	140	AACATCATGATTTTATGATGTCGCTAAGCGGGGCTCTCAGGGGTCTCTGATCGGCTTCTCTGGCT	199
D _b	121	AACATCATGATTTTATGAGGCGCAGTAAGCGGCGCTCTCAGGGGTCTCTAATCGGCTTCTCTGGCT	180
Q _y	200	CCAAGTCTGGCAACACGGCGCTCCCTGACCATCTCTGGGCTCCAGGCTCAGGACGAGCGTG	259
D _b	181	CCAAGTCTGGCAACACGGCGCTCCCTGACCATCTCTGGGCTCCAGGCTCAGGACGAGCGTG	240
Q _y	260	ATTATTACTGTGTTGTTTCATATACAACAGTAGCACTTT	296
D _b	241	ATTATTACTGTGCTCATATGCAAGTAGTACACTTT	277

RESULT 12

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US-10-029-386-15224/c
: Sequence 15224, Application US/10029386
: Publication No. US20030194704A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Bank, David R.
: APPLICANT: Hanzel, David K.
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
: FILE OF INVENTION: EXPRESSION ANALYSIS TWO
: FILE REFERENCE: AEOmica-X-2
: CURRENT APPLICATION NUMBER: US/10/029,386
: CURRENT FILING DATE: 2001-12-20
: NUMBER OF SEQ ID NOS: 34288
: SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
: SEQ ID NO 15224
: LENGTH: 278
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO CHR22_117.0
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
: OTHER INFORMATION: SWISSPROT HIT: P01709, EVALUOE 1.00e+30
: OTHER INFORMATION: NT HIT: X57825.1, EVALUOE 0.00e+00
: OTHER INFORMATION: EST_HUMAN HIT: BG759257.1, EVALUOE 5.00e-99
: US-10-029-386-15224

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Query Match	65.9%	Score 219.6;	DB 15;	Length 278;
Best Local Similarity	89.1%	Pred. No. 8.1e-65;		
Matches 237; Conservative	0;	Mismatches 29;	Indels	0; Gaps 0;

Qy	1	CAGTCGCCCCGACTCAGCCTCCCTCTGTGTCGGGTCTCTCGACAGTCGGTGACCATC	60
Db	267	CAGTCGCCCCGACTCAGCCTCCCTCTGTGTCGGGTCTCTCGACAGTCAGTCAGCATC	208
Qy	61	TCCTGACTGGAAACAGCGAGTACGTTGTGTGGTTTAACTATATGTCTCCTGGTACCACAC	120
Db	207	TCTGCACTGGAACACGAGTGTGTGGAGTTATGACTATGTCTCTGTGTACCACAG	148
Qy	121	CACCCAGGAAAGCCCCAAACTCATGATTTATCATGTCTGCTAAGCGGGGCTCAGGGGTC	180
Db	147	CACCCAGGCACAGTCCCCAAACCCATGATCTCAATGTCAATATCAGCCCTCAGGGGTC	88
Qy	181	TCTGATCGCTCTCTGGTCTCCAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGGTC	240
Db	87	CTGTATCGTTTCTCTGGCTCCAGTCTGGCAATACGGCTCCATGACCATCTCTGGACTC	28
Qy	241	CAGCGTGAGGACGAGCGCTGATTTATTA	266
Db	27	CAGGCTGAGGACGAGCGCTGATTTATTA	2

RESULT 13

RESULT 13

```

US-09-734-613-15
; Sequence 15, Application US/09734613
; Publication No. US20020088016A1
; GENERAL INFORMATION:
; APPLICANT: BRUGGEMANN, Marianne
; TITLE OF INVENTION: MURINE EXPRESSION OF A HUMAN IGA LAMBDA LOCUS
; FILE REFERENCE: 37945-0009
; CURRENT APPLICATION NUMBER: US/09/734,613
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03632
; PRIOR FILING DATE: 1999-11-03
; PRIOR APPLICATION NUMBER: GB 9823930.4
; PRIOR FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-734-613-15

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Query Match 65.6%; Score 218.4; DB 13; Length 246;
Best Local Similarity 93.4%; Pred. No. 2e-64;
Matches 228; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy	53	TCACCATCTCTGCACGTGGAAACGAGCGATGACGTTGGTGTATTAACATATGCTCTCTGGT	112
Db	2	TCACCATCTCTGCACGTGGAAACGAGCGATGACGTTGGTGTATTAACATATGCTCTCTGGT	61
Qy	113	ACCAACACCAACCCAGGCGAAAGCCCCCAAACTCATGATTTATGATGTCGCTTAAGCGGCGCT	172
Db	62	ACCAACAGCAACCCAGGCGAAAGCCCCCAAACTCATGATTTATGAGGTCAGTAATCGGCGCT	121
Qy	173	CAGGGTCTCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCTCCCTGACCATCT	232
Db	122	CAGGGTTCTTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCTCCCTGACCATCT	181
Qy	233	CTGGGCTCCAGGCTGAGGACGAGGCTGATTTACTGTTGTCATATACAAACAGTAGCA	292
Db	182	CTGGGCTCCAGGCTGAGGACGAGGCTGATTTACTGAGCTCATATACAGCAGCAGCA	241
Qy	293	CTTT	296
Db	242	CTCT	245

RESIT.T 14

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US-09-734-613-16
; Sequence 16, Application US/09734613
; Publication No. US2002098016A1
; GENERAL INFORMATION:
; APPLICANT: BRUGEMANN, Marianne
; TITLE OF INVENTION: MURINE EXPRESSION OF A HUMAN IGA LAMBDA LOCUS
; FILE REFERENCE: 37945-0009
; CURRENT APPLICATION NUMBER: US/09/734,613
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03632
; PRIOR FILING DATE: 1999-11-03
; PRIOR APPLICATION NUMBER: GB 9823930.4
; PRIOR FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-734-613-16

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Query Match      64.5%; Score 214.8; DB 13; Length 243;
Best Local Similarity 93.0%; Pred. No. 3.4e-63;
Matches 225: Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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53 TCACCATCTCCTGCACCTGGAAACAGCGATGACGTTGGTGGTTAATACTATGTCTCCTGGT 112

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: June 19, 2004, 03:12:07 ; Search time 1733 Seconds
(without alignments)
5738.088 Million cell updates/sec
Title: US-09-019-441A-1_COPY_58_390
Perfect score: 333
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 10684158
Minimum DB seq length: 0
Maximum DB seq length: 333
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_estc.*
9: gb_estl.*
10: gb_est2.*
11: gb_estc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_irv.*
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20: em_gss_vrt.*
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29: gb_gss2.*

217.6 65.3 260 14 T27942
215.6 64.7 307 10 BF825613
214.8 64.5 327 14 CD703327
213.8 64.2 296 14 CD698983
213.4 64.1 313 9 AA327392
212 63.7 327 14 CD6989821
211.2 63.4 323 10 AW404118
211 63.4 243 13 BU584479
210 63.1 234 13 BU584573
209.8 63.0 284 13 BU584480
206.2 61.9 254 10 AW407182
206 61.9 318 13 BX283257
205.4 61.7 248 13 BU584608
205 61.6 282 10 BE706848
203 61.0 320 13 BU584244
202.2 60.7 328 14 CD695826
202 60.4 237 13 BU584067
201 60.4 251 14 N47367
199.4 59.9 333 12 BP431103
198.4 59.6 244 14 H22217
192.2 57.7 291 13 BU584284
191.2 57.4 314 9 AA327386
189.2 56.8 325 14 CD700666
189.2 56.8 287 13 BU584265
188.4 56.6 310 13 BU584281
188 56.5 313 12 BP430005
185.8 55.8 293 13 BU584332
183.6 55.1 214 13 BU584098
183.6 55.1 294 13 BU584145
183.2 55.0 235 10 AW806367
183 55.0 281 13 BU584254
180.2 54.1 217 13 BU584110
179.8 54.0 307 10 AW407310
178.8 53.7 309 13 BU584379
177 53.2 309 12 BP429773
175 52.6 285 13 BU584279
175 52.6 315 12 BM823400
174.4 52.4 331 14 CD692574
173.6 52.1 280 13 BU584640
173 52.0 221 10 AW407470
173 52.0 305 12 BP429335

ALIGNMENTS

RESULT 1
CD707555
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD707555 325 bp mRNA linear EST 25-JUN-2003
EST24082 human nasopharynx Homo sapiens cDNA, mRNA sequence.
CD707555
CD707555.1 GI:32238185
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 325)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsuns.edu.cn.

FEATURES
source
1..325
/organism="Homo sapiens"
/mol_type="mRNA"

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	237.6	71.4	325	14	CD707555 EST24082
2	231.4	69.5	280	13	BU584333 3392316H1
3	224.4	67.4	258	13	BU584280 3045436H1
4	219.8	66.0	248	14	CD705383 EST21910

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 71.4%; Score 237.6; DB 14; Length 325;
Best Local Similarity 94.6%; Pred. No. 7.7e-57;
Matches 246; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCCTCCCTGTGTCTGGGTCCTCTGGACAGTCGGTCCACATC 60
DB 66 CAGTCTGCCCGACTCAGCCCTCCCTGTGTCTGGGTCCTCTGGACAGTCGGTCCACATC 125
QY 61 TCTGCACTGGAACACAGCAGTACGTTGGTGGTATTAATATGTCCTCTGGTACCAACAC 120
DB 126 TCTGCACTGGAACACAGCAGTACGTTGGTGGTATTAATATGTCCTCTGGTACCAACAC 185
QY 121 CACCCAGGCAAGCCCCCAACTCATGATTTATGATGTCGCTTAAGCGGCTCAGGGTC 180
DB 186 GACCCAGGCAAGCCCCCAACTCATGATTTATGATGTCGCTTAAGCGGCTCAGGGTC 245
QY 181 TCTGATCGCTTCTGCTGCCAAGTCTGCAACAGGCTCCCTGACCATCTCTGGGCTC 240
DB 246 TCTAATCGCTTCTGCTGCCAAGTCTGCAACAGGCTCCCTGACCATCTCTGGGCTC 305
QY 241 CAGGCTGAGGACGAGGCTGA 260
DB 306 CAGGCTGAGGACGAGGCTGA 325

RESULT 2
BU584333 280 bp mRNA linear EST 20-SEP-2002
LOCUS 3392316H1 LUNGNOT28 Homo sapiens cDNA clone 3392316 5', mRNA
DEFINITION
sequence.
ACCESSION BU584333
VERSION BU584333.1 GI:23258298
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 280)
AUTHORS Collins,J.E., Goward,M.E., Cole,C.G., Smink,L.J., Huckle,E.J.,
Knowles,S., Bye,J.M., Beare,D.M. and Dunham,I.
TITLE Re-evaluating Human Gene Annotation: A Second Generation Analysis
of Chromosome 22
JOURNAL Unpublished (2002)
COMMENT Contact: Panzer SR
Incyte Genomics, Inc.
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 845 4682
Fax: 650 845 5495
Email: spanzer@incyte.com.
Location/Qualifiers
1..280
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="3392316"
/tissue_type="lung"
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/note="lung, mw/adenoCA, 53M, m/LUNGUT17"

FEATURES
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Query Match 69.5%; Score 231.4; DB 13; Length 280;
Best Local Similarity 92.1%; Pred. No. 4.1e-55;
Matches 244; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCCTCCCTGTGTCTGGGTCCTCTGGACAGTCGGTCCACATC 60

ORIGIN
Query Match 57.4%; Score 224.4; DB 13; Length 258;
Best Local Similarity 91.9%; Pred. No. 3.9e-53;
Matches 237; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 30 GTCTGGGTCCTCTGGACAGTCGGTCCACCATCTCTGCACTGGAACACAGGATGACGTTGG 89
DB 1 GTCCGGGTCCTCTGGACAGTCAGTCACCATCTCTGCACTGGAACACAGGATGACGTTGG 60
QY 90 TGGTTATTAATATGTCCTCTGGTACCAACACCCAGGCAAGGCCCCCAACTCATGAT 149
DB 61 TCGTTATAAATATGTCCTCTGGTACCAACACCCAGGCAAGGCCCCCAACTCATGAT 120
QY 150 TTATGATTCGCTAAGCGGCTCAGGGGTCCTGATGTCGCTTCTCTGGCTCCAAAGTCGG 209
DB 121 TTATGAGGTGAGTAAAGCGGCTCAGGGGTCCTGATGTCGCTTCTCTGGCTCCAAAGTCGG 180
QY 210 CAACACGGCTCCCTGACCATCTCTGGGTCCTGAGGTCAGGACAGGCTGATTAATCTG 269
DB 181 CAACACGGCTCCCTGACCATCTCTGGGTCCTGAGGTCAGGATGAGGCTGCTTATTACTG 240
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QY 270 TTGTTTCATATACACACG 287
Db 241 CTGCTCATTTACAGCAG 258

RESULT 4
CD705383 248 bp mRNA linear EST 25-JUN-2003
LOCUS EST21910 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION CD705383
ACCESSION CD705383
VERSION CD705383.1 GI:32236013
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 248)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Vixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES
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library from southern Chinese"

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Best Local Similarity 93.1%; Pred. No. 7.8e-52;
Matches 230; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 CAGTGTGCCCCGATCAGCTCCCTCTGTCGTGGTCTCTGACAGTGGTCAACCATC 60
Db 2 CAGTGTGCCCCGATCAGCTCCCTCTGTCGTGGTCTCTGACAGTGGTCAACCATC 61

QY 61 TCCTGCACTGGAACAGCAGATGAGTGGTGGTATTAACTATGTCCTCTGTTACCAAC 120
Db 62 TCCTGCACTGGAACAGCAGATGAGTGGTGGTATTAACTATGTCCTCTGTTACCAAC 121

QY 121 CACCAGGCAAGCCCCCAAACTCATGATTTATGATGCGTAAGCGGCTCAGGGGTC 180
Db 122 CACCAGGCAAGAACCAAACTCATGATTTATGCTGTAATCGGCCCTCAGGGGTT 181

QY 181 TCTGATCCCTTCTCTGGTCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240
Db 182 TCTAATCCCTTCTCTGGTCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 241

QY 241 CAGGCTG 247
Db 242 CAGGCTG 248

RESULT 5
T27942 260 bp mRNA linear EST 06-SEP-1995
LOCUS EST20865 Human Spleen Homo sapiens cDNA 5' end similar to
DEFINITION immunoglobulin lambda light chain V.J.C regions (GB:L03633)
(HT:3223), mRNA sequence.
ACCESSION T27942
VERSION T27942.1 GI:610040

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EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 260)
AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Pitdegald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkler, P.S.,
Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palacios, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegri, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A.,
Coleman, J.A., Collins, B.-J., Dimke, D., Feng, P., Ferrie, A.,
Fischer, C.A., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Jh, H., Li, H.,
Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
JOURNAL Nature 377, 3-174 (1995)
MEDLINE 96026280
PUBMED 7566098
COMMENT Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
Seq primer: M3 Reverse.
FEATURES
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Best Local Similarity 89.6%; Pred. No. 3.4e-51;
Matches 232; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 34 GGCTCTCCCTGGACAGTGGTTCACCATCTCTGACACAGGACCAAGCCCAACATCATGATTAT 93
Db 2 GGCTCTCCCTGGACAGTGGTTCACCATCTCTGACACAGGACCAAGCCCAACATCATGATTAT 91

QY 94 TATAAATATGTTCTCTGGTACCAACACCAAGCCCAAGCCCAACATCATGATTAT 153
Db 62 TATAAATGTTCTCTCTGGTACCAAGCCCAAGCCCAAGCCCAACATCATGATTAT 121

QY 154 GATGTCGCTAAGCGGCTCTGAGGCTCTGATGCTGCTCTGCTCCCAAGCTGGCAAC 213
Db 122 GAGTCAGTAAATCGGCCCTCAGGGGCTCCCTGATGCTCTCTGCTCCCAAGCTGGCAAC 181

QY 214 ACGGCTCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATGTTGT 273
Db 182 ACGGCTCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATGTTGT 241

QY 274 TCATATACACACAGTAGCA 292
Db 242 TCATATACACACAGCA 260

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ACCESSION	CD598983	1	GI:32227826
VERSION	EST.		
KEYWORDS	Homo sapiens (human)		
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1. (bases 1 to 296)		
AUTHORS	Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-X., Pan, Z.-G. and Zeng, Y.-X.		
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: YiXin Zeng Cancer Center Sun Yat-sen University 651 Dongfeng Road East, Guangzhou 510060, China Tel: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@gzsums.edu.cn.		
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	/clone_lib="human nasopharynx"		
	/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"		
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Best Local Similarity	89.5%;	Pred. No. 4.4e-50;	
Matches 230;	Conservative	0;	Mismatches 27; Indels 0; Gaps 0;
QY	1	CAGTCTGCCCGACTCAGCTCCCTCTGCTCTGCTGGGTCTCTGACAGTGGTACCAAC	60
DB	40	CAGTCTGCCCTGACTCAGCTGGCTCCGCTGCTGGGTCTCTGACAGTGGTACCAAC	99
QY	61	TCTGTCACTGGCAACACAGCGATGAGCTTGGTGGTTATTAATGATGCTCTGGTACCAAC	120
DB	100	TCTGTCACTGGCAACACAGTGAATGTTGGAGTCTATGCTGGTCTCTGGTACCAAC	159
QY	121	CACCCAGGAAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGGCTCTAGGGGCT	180
DB	160	CACCCAGGAAAGCCCCCAACTCATCATTTATAAGGGCTATTAACCGGCGCTTCAGGGG	219
QY	181	TCTGTATGCTTCTCTGCTCTCAAGTCTGGCAACACAGCGCTCCCTGACCATCTCTGGGCT	240
DB	220	TCTATGCTTCTCTGCTCTCAAGTCTGGCAACACAGCGCTCCCTGACCATCTCTGGGCT	279
QY	241	CAGCTGTAGCAGGAGGC	257
DB	280	CAGCTGTAGCAGGAGGC	296
RESULT 9			
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LOCUS	EST30721	Colo I Homo sapiens cDNA 5' end similar to	linear EST 20-APR-1997
DEFINITION	immunoglobulin lambda chain, mRNA sequence.		
ACCESSION	AA327392		
VERSION	AA327392.1	GI:1979637	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1. (bases 1 to 313)		
	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,		
	Bult, C.C., Lee, N.H., Kirkness, E.F., Weinschenk, K.G., Gockayne, J.D.,		
	White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,		
	Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,		
	Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,		

ACCESSION CD698821 GI:32227508
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 327)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn

FEATURES
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/lab_host="DH10B (LT1)"
/clone_lib="NIH MGC 37"
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 63.7%; Score 212; DB 14; Length 327;
Best Local Similarity 88.5%; Pred. No. 1.5e-49; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1 CAGCTGCCCCGACTCAGCTCCCTCTGTGTCTGGGTCTCTCGACAGTCGGTCCACATC 60
DB 68 CAGCTGCGGTGACTCAGCTCGCTCGCTGTGTGTCTGGGTCTCTCGACAGTCGGTCCACATC 127
QY 61 TCCTGCACTGAACCGCGATGAGTGTGTGTATTAATGCTCTCTGTATCAACAC 120
DB 128 TCATGCACTGAACCGCGATGAGTGTGTGTATTAATGCTCTCTGTATCAACAC 187
QY 121 CACCAGCAAGCCGCCAACTCATGATTTATGATTCGTAATGCGCGGCTCAGGGGTC 180
DB 188 CACCAGCAAGCCGCCAACTCATGATTTATGATTCGTAATGCGCGGCTCAGGGGTC 247
QY 181 TCTGATCGTCTCTGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
DB 248 TCTAATCGCTTCTCTGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 307
QY 241 CAGGCTGAGGACGAGGCTGA 260
DB 308 CGGCTGAGGACGAGGCTGA 327

RESULT 11
AM404118
LOCUS
DEFINITION UI-EP-BL0-abu-b-04-0-UI.r1 NIH MGC_37 Homo sapiens cDNA clone
IMAGE:3057727 5', mRNA sequence.
ACCESSION AM404118
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 323)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
Location/Qualifiers
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/lab_host="DH10B (LT1)"
/clone_lib="NIH MGC 37"
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 63.4%; Score 211.2; DB 10; Length 323;
Best Local Similarity 86.2%; Pred. No. 2.6e-49; Indels 12; Gaps 1;
Matches 250; Conservative 0; Mismatches 28; Indels 12; Gaps 1;
QY 1 CAGCTGCCCCGACTCAGCTCCCTCTGTGTCTGGGTCTCTCGACAGTCGGTCCACATC 60
DB 39 CAGCTGCCCCGACTCAGCTCCCTCTGTGTCTGGGTCTCTCGACAGTCGGTCCACATC 98
QY 61 TCCTGCACTGGAACCGAGCATGAGTGTGTGTATTAATGCTCTCTGTATCAACAC 120
DB 99 TCCTGCACTGGAACCGAGCATGAGTGTGTGTATTAATGCTCTCTGTATCAACAC 146
QY 121 CACCAGCAAGCCGCCAACTCATGATTTATGATTCGTAATGCGCGGCTCAGGGGTC 180
DB 147 CACCAGCAAGCCGCCAACTCATGATTTATGATTCGTAATGCGCGGCTCAGGGGTC 206
QY 181 TCTGATCGTCTCTGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
DB 207 TCTAATCGCTTCTCTGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 266
QY 241 CAGGCTGAGGACGAGGCTGATTTACTGTTGTTATATACCAACAGTAG 290
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RESULT 12
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4633268E1 GELADIT02 Homo sapiens cDNA clone 4633268 5', mRNA
sequence.
ACCESSION BU584479
VERSION BU584479.1 GI:23258444
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 243)
AUTHORS Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Collins, J.E., Goward, M.E., Cole, C.G., Smink, L.J., Huckle, E.J.,
Knowles, S., Bye, J.M., Beare, D.M. and Dunham, I.
Re-evaluating Human Gene Annotation: A Second Generation Analysis
of Chromosome 22
JOURNAL Unpublished (2002)
COMMENT Contact: Panzer SR
Incyte Genomics, Inc.
3160 Porter Drive, Palo Alto, CA 94304, USA

ACCESSION CD698821 GI:32227508
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 327)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn

FEATURES
source
1..327
/organism="Homo sapiens"
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/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 63.7%; Score 212; DB 14; Length 327;
Best Local Similarity 88.5%; Pred. No. 1.5e-49; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1 CAGCTGCCCCGACTCAGCTCCCTCTGTGTCTGGGTCTCTCGACAGTCGGTCCACATC 60
DB 68 CAGCTGCGGTGACTCAGCTCGCTCGCTGTGTGTCTGGGTCTCTCGACAGTCGGTCCACATC 127
QY 61 TCCTGCACTGAACCGCGATGAGTGTGTGTATTAATGCTCTCTGTATCAACAC 120
DB 128 TCATGCACTGAACCGCGATGAGTGTGTGTATTAATGCTCTCTGTATCAACAC 187
QY 121 CACCAGCAAGCCGCCAACTCATGATTTATGATTCGTAATGCGCGGCTCAGGGGTC 180
DB 188 CACCAGCAAGCCGCCAACTCATGATTTATGATTCGTAATGCGCGGCTCAGGGGTC 247
QY 181 TCTGATCGTCTCTGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
DB 248 TCTAATCGCTTCTCTGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 307
QY 241 CAGGCTGAGGACGAGGCTGA 260
DB 308 CGGCTGAGGACGAGGCTGA 327

RESULT 11
AM404118
LOCUS
DEFINITION UI-EP-BL0-abu-b-04-0-UI.r1 NIH MGC_37 Homo sapiens cDNA clone
IMAGE:3057727 5', mRNA sequence.
ACCESSION AM404118
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 323)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tel: 650 845 4682

Fax: 650 845 5495

Email: spanzer@incyte.com.

Location/Qualifiers

FEATURES

source

1..243

/organism="Homo sapiens"

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/db_xref="taxon:9606"

/clone="4633268"

/tissue_type="gallbladder"

/clone_lib="GBLADIT02"

/note="gallbladder, cholecystitis, cholelithiasis, 18F"

ORIGIN

Query Match

Best Local Similarity 63.4%; Score 211; DB 13; Length 243;

Matches 223; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY

49 TCGGTACCAATCTCTGCACTGGAAACCGGATGACGTTGGTGGTTATTAACATATGCTCC 108

DB

1 TCGATCACCATCTCTGCACTGGAAACCGGATGACGTTGGTGGTTATTAACATATGCTCC 60

QY

109 TGGTACCAACACCCAGGCAAGCCCAACCTCATGATTTATGATGCTGCTAAGCGG 168

DB

61 TGGTACCAACACCCAGGCAAGCCCAACCTCATGATTTATGATGCTGCTAAGCGG 120

QY

169 GCCTCAGGGGTTCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACC 228

DB

121 CCCTCAGGGGTTCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACC 180

QY

229 ATCTCTGGCTCCAGGCTGAGCAGGCTGATTTACTGTTTATATACAAACAGT 288

DB

181 ATCTCTGGCTCCAGGCTGAGCAGGCTGATTTACTGATCTATATGCACTCATATCAAGTAGT 240

QY

289 AGC 291

DB

241 AGC 243

RESULT 13

BU584573

LOCUS

5559803H1 BRSTDIT01 Homo sapiens cDNA clone 5559803 5', mRNA

DEFINITION

sequence.

ACCESSION

BU584573

VERSION

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 234)

Collins,J.E., Goward,M.E., Cole,C.G., Smink,L.J., Huckle,E.J.,

Knowles,S., Bye,J.M., Beare,D.M. and Dunham,I.

Re-evaluating Human Gene Annotation: A Second Generation Analysis

of Chromosome 22

Unpublished (2002)

Contact: Panzer SR

Incyte Genomics, Inc.

3160 Porter Drive, Palo Alto, CA 94304, USA

Tel: 650 845 4682

Fax: 650 845 5495

Email: spanzer@incyte.com.

Location/Qualifiers

1..234

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="5559803"

/tissue_type="breast"

/clone_lib="BRSTDIT01"

/note="breast, PF changes, mw/intraductal cancer, 48F"

ORIGIN

Query Match

Best Local Similarity 63.1%; Score 210; DB 13; Length 234;

Matches 219; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY

49 TCGGTACCAATCTCTGCACTGGAAACCGGATGACGTTGGTGGTTATTAACATATGCTCC 108

DB

1 TCGATCACCATCTCTGCACTGGAAACCGGATGACGTTGGTGGTTATTAACATATGCTCC 60

QY

109 TGGTACCAACACCCAGGCAAGCCCAACCTCATGATTTATGATGCTGCTAAGCGG 168

DB

61 TGGTACCAACACCCAGGCAAGCCCAACCTCATGATTTATGATGCTGCTAAGCGG 120

QY

169 GCCTCAGGGGTTCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACC 228

DB

121 CCCTCAGGGGTTCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACC 180

QY

229 ATCTCTGGCTCCAGGCTGAGCAGGCTGATTTACTGTTTATATACAAACAGT 282

DB

181 ATCTCTGGCTCCAGGCTGAGCAGGCTGATTTACTGATCTATATGCACTCATATCAAGTAGT 234

RESULT 14

BU584480

LOCUS

4633413H1 GBLADIT02 Homo sapiens cDNA clone 4633413 5', mRNA

DEFINITION

sequence.

ACCESSION

BU584480

VERSION

EST.

KEYWORDS

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 264)

Collins,J.E., Goward,M.E., Cole,C.G., Smink,L.J., Huckle,E.J.,

Knowles,S., Bye,J.M., Beare,D.M. and Dunham,I.

Re-evaluating Human Gene Annotation: A Second Generation Analysis

of Chromosome 22

Unpublished (2002)

Contact: Panzer SR

Incyte Genomics, Inc.

3160 Porter Drive, Palo Alto, CA 94304, USA

Tel: 650 845 4682

Fax: 650 845 5495

Email: spanzer@incyte.com.

Location/Qualifiers

1..264

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="4633413"

/tissue_type="gallbladder"

/clone_lib="GBLADIT02"

/note="gallbladder, cholecystitis, cholelithiasis, 18F"

ORIGIN

Query Match

Best Local Similarity 63.0%; Score 209.8; DB 13; Length 264;

Matches 237; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

QY

50 CGGTACCAATCTCTGCACTGGAAACCGGATGACGTTGGTGGTTATTAACATATGCTCC 109

DB

1 CGATCACCATCTCTGCACTGGAAACCGGATGACGTTGGTGGTTATTAACATATGCTCC 60

QY

110 GGTACCAACACCCAGGCAAGCCCAACCTCATGATTTATGATGCTGCTAAGCGG 169

DB

61 GGTACCAACACCCAGGCAAGCCCAACCTCATGATTTATGATGCTGCTAAGCGG 120

QY

170 CCTCAGGGGTTCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCA 229

DB

121 CCTCAGGGGTTCTGAT-6CTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCA 179

QY 230 TCTCTGGGCTCCAGGCTGAGGACGAGCTGATTATTACTGTGTTCATATACACACAGTA 289
Db 180 TCTCTGGGCTCCAGGCTGAGGACGAGCTGATTATTATTGCAACTCATATACAGTAGTA 239
QY 290 GCACCTTTCTTATTCGGAAGAGGAC 314
Db 240 GCACTCCAGTCTTCGGAAGACTGGAC 264

RESULT 15

AW407182 254 bp mRNA linear EST 16-FEB-2000
LOCUS
DEFINITION UI-HF-BL0-ade-g-06-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3061427 5', mRNA sequence.

ACCESSION AM407182
VERSION
KEYWORDS
SOURCE EST.
AW407182.1 GI:6926239

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 254)

NIH-MGC <http://mhc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.lnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

FEATURES

source

Location/Qualifiers

1..254

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone IMAGE:3061427"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (LTI)"

/clone_lib="NIH_MGC_37"

/note="Vector: pMT3-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(1.5-2.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 61.9%; Score 206.2; DB 10; Length 254;

Best Local Similarity 94.3%; Pred. No. 6e-48;

Matches 214; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 CAGTGTGCCCGACTCAGCCCTCCTCTGTGTGGGTCTCTGGACAGTGGTCAACATC 60
Db 28 CAGTGTGCCCTGACTCAGCTGCTCTGGTCTCTGGACAGTGGTCAACATC 87

QY 61 TCCTGCACTGAACAGCAGGATGGTGGTATTACTATGTCTCTGGTACCAACAC 120
Db 88 TCCTGCACTGAACAGCAGGATGGTGGTATTACTATGTCTCTGGTACCAAC 147

QY 121 CACCAGCAAGCCCAAACTCATGATTTATGATGTGCTAAGCGGGCTCAGGGGTC 180
Db 148 CACCAGCAAGCCCAAACTCATGATTTATGATGTGCTAAGCGGGCTCAGGGGTT 207

QY 181 TCTGATCGCTTCTCTGGCTCCAGTCTGGCAACAGGGCTCCCTGAC 227
Db 208 TCTAATCGCTTCTCTGGCTCCAGTCTGGCAACAGGGCTCCCTGAC 254

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 05:42:35 ; Search time 1845 Seconds
(without alignments)
8833.052 Million cell updates/sec

Title: US-09-019-441A-3_COPY_48_423

Perfect score: 376

Sequence: 1 ggtctgtccacagctgcagc.....tccctggtaacogtctctca 376

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 3186280

Minimum DB seq length: 0
Maximum DB seq length: 376

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.vi.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Match	Length	DB ID	Description
1	275.6	73.3	373	9	MMU57558
2	270	71.8	363	9	MMU57559
3	268.4	71.4	363	9	MMU57559
4	268.4	71.4	363	9	MMU57559
5	263.4	70.1	366	9	MMU57559
6	263	69.9	368	9	MMU57559
7	260.4	69.3	363	9	MMU57559
8	257.2	68.4	363	9	MMU57559
9	255.6	68.0	363	9	MMU57559
10	255.6	68.0	363	9	MMU57559
11	255.4	67.9	366	9	MMU57559
12	254.2	67.6	364	9	MMU57559
13	254	67.6	375	9	MMU57559
14	253	67.3	364	9	MMU57559
15	252.4	67.1	363	9	MMU57559
16	252.2	67.1	366	9	MMU57559
17	251.4	66.9	312	9	MMU57559
18	250	66.5	354	9	MMU57559
19	248.4	66.1	354	9	MMU57559
20	247.8	65.9	308	9	MMU57559
21	247.6	65.9	360	9	MMU57559
22	247.6	65.9	375	9	MMU57559
23	247.4	65.8	363	9	MMU57559
24	246.4	65.5	357	9	MMU57559
25	246	65.4	360	9	MMU57559
26	245.8	65.4	366	9	MMU57559
27	245.6	65.3	369	9	MMU57559
28	244.6	65.1	372	6	MMU57559
29	244.6	65.1	375	9	MMU57559
30	244.4	65.0	360	9	MMU57559
31	244.2	64.9	366	9	MMU57559
32	244	64.9	369	9	MMU57559
33	243.6	64.8	365	9	MMU57559
34	243.2	64.7	354	6	MMU57559
35	243	64.6	372	9	MMU57559
36	242.8	64.6	371	9	MMU57559
37	242.6	64.5	366	9	MMU57559
38	242	64.4	317	9	MMU57559
39	242	64.4	357	9	MMU57559
40	241.8	64.3	363	9	MMU57559
41	241.4	64.2	296	6	MMU57559
42	241.2	64.1	360	9	MMU57559
43	241.2	64.1	363	9	MMU57559
44	240.2	63.9	322	9	MMU57559
45	240.2	63.9	351	9	MMU57559

ALIGNMENTS

RESULT 1
LOCUS MMU57558 373 bp mRNA linear PRI 02-OCT-1996
DEFINITION Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC antibody, mRNA, partial cds.
ACCESSION U57558
VERSION U57558.1 GI:1575063
KEYWORDS
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 373)
AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.

KEYWORDS Igm; Igm heavy chain; immunoglobulin mu heavy chain; variable region.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE AUTHORS Chiorazzi, N. and Ferrarini, M.

TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)

MEDLINE 20281644

PUBMED 10820234

REFERENCE 2 (bases 1 to 363)

AUTHORS Dono, M.

TITLE Direct Submission

JOURNAL Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY

FEATURES source

1..363

/organism="Homo sapiens"

/mol_type="rRNA"

/db_xref="taxon:9606"

/chromosome="14"

/clone="CD2716w-2"

/cell_type="Igd-low, SE B-lymphocyte"

/tissue_type="tonsil"

/rearranged

1..363

/gene="IGHV4-4"

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/gene="IGHV4-4"

/codon_start=1

/product="immunoglobulin mu heavy chain variable region"

/protein_id="CAB66344.1"

/db_xref="GI:6723526"

/db_xref="REMBL:CAB66344"

/translation="QVQLQESGPGLVKPSGTLSTLCAVSGGISSSNWSWVRPPGK GLEWIGEIVHSGSTNPNLSKSRVTISVDTSKQFSLKLSSTAAADTAVYCAADSYI FWSGKGVWGQGLTVTVSS"

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/product="immunoglobulin mu heavy chain variable region"

ORIGIN

Query Match 71.4%; Score 268.4; DB 9; Length 363;

Best Local Similarity 85.2%; Pred. No. 2.6e-64;

Matches 312; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

QY 11 CAGCTGCAGCTGCAGAGTCCGCGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 70

DB 1 CAGGTGCAGCTGCAGAGTCCGCGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60

QY 71 ACCTGGCTGTCTCTGTGGTCTCTCTCAGAGTAGTAACTGTGGAGCCTGGATCCGCCAG 130

DB 61 ACCTGGCTGTCTCTGTGGTCTCTCTCAGAGTAGTAACTGTGGAGTGGATCCGCCAG 120

QY 131 CCCCAGAGGAGGAGTGGAGTGGATCTCTGTGGTGGAGTGGAGTGGAGTGGAGTGGAGT 190

DB 121 CCCCAGAGGAGGAGTGGAGTGGATCTCTGTGGTGGAGTGGAGTGGAGTGGAGTGGAGT 177

QY 191 TACAACCCGTCCTCAAGAGTGGAGTGGATCTCTGTGGTGGAGTGGAGTGGAGTGGAGTGGAGT 250

DB 178 TACAACCCGTCCTCAAGAGTGGAGTGGATCTCTGTGGTGGAGTGGAGTGGAGTGGAGTGGAGT 237

QY 251 TCCCTGACCTGAACCTGTGACCCGCGGACAGCGCGGTATTAATCTGTGGAGTGGAGTGGAGT 310

DB 238 TCCCTGACCTGAGCTGTGTGAGCTGCCGAGACAGCGCGGTATTAATCTGTGGAGTGGAGTGGAGT 297

QY 311 TGGGCCCCAAATAGCTCGAACAAACGCTAGTCTCTGGGCGCCAGGAGTCTCTGTGGTGGAGTGGAGT 370

Db 298 TCGTATTACGAATTTTGGAGTGGAAAGAGTCTGGGGCCAGGGCACCCCTGGTCAACCGTC 357

QY 371 TCCTCA 376

DB 358 TCCTCA 363

RESULT 4

HSU80179

LOCUS Human immunoglobulin heavy chain variable region (V4-4b) gene, partial cds.

DEFINITION Human immunoglobulin heavy chain variable region (V4-4b) gene, partial cds.

ACCESSION U80179

VERSION U80179.1

KEYWORDS GI:1791200

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 363)

AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.

TITLE Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient

JOURNAL Clin. Exp. Immunol. 107 (2), 372-380 (1997)

MEDLINE 97182739

PUBMED 9030878

REFERENCE 2 (bases 1 to 363)

AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.B.

TITLE Direct Submission

JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA

FEATURES source

1..363

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="14"

/map="14q32-q33"

/clone="tt2h7"

/cell_type="CD19+ B cells"

/tissue_type="peripheral blood"

/notes="CD19+ peripheral blood B cells obtained from a healthy subject; clone 104 in reference 1"

1..363

/gene="V4-4b"

<1..>363

/gene="V4-4b"

/notes="Ig VH4 heavy chain"

/codon_start=1

/product="immunoglobulin heavy chain variable region"

/protein_id="AAC51094.1"

/db_xref="GI:1791201"

/translation="QVQLQESGPGLVKPSGTLSTLCAVSGGISSSNWSWVRPPGK GLEWIGEIVHSGSTNPNLSKSRVTISVDTSKQFSLKLSSTAAADTAVYCAARGIPH DYTLPDYWGQGLTVTVSS"

ORIGIN

Query Match 71.4%; Score 268.4; DB 9; Length 363;

Best Local Similarity 85.2%; Pred. No. 2.6e-64;

Matches 312; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

QY 11 CAGCTGCAGCTGCAGAGTCCGCGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 70

DB 1 CAGGTGCAGCTGCAGAGTCCGCGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60

QY 71 ACCTGGCTGTCTCTGTGGTCTCTCTCAGAGTAGTAACTGTGGAGCCTGGATCCGCCAG 130

DB 61 ACCTGGCTGTCTCTGTGGTCTCTCTCAGAGTAGTAACTGTGGAGTGGATCCGCCAG 120

QY 131 CCCCAGAGGAGGAGTGGAGTGGATCTCTGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 190

DB 121 CCCCAGAGGAGGAGTGGAGTGGATCTCTGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 177

QY 191 TACAAACCGTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACAGTCCTCAAGAACCAAGTTC 250
Db 178 TACAACCGTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACAGTCCTCAAGAACCAAGTTC 237
QY 251 TCCCTGACCTGACCTGTCAGCCGCGGACAGCCGCTGATTACTGTCGACAGAT 310
Db 238 TCCCTGACCTGACCTGTCAGCCGCGGACAGCCGCTGATTACTGTCGACAGAT 297
QY 311 TGGGCCCCAAATAGCTGGAACACGCTAGGCTTCTGGGCCCCAGGAGTCTTGTCACCGTC 370
Db 298 ATCCCGCATGACTAGCGCACCTCTTTGACTACTGGGCCCCAGGAGTCTTGTCACCGTC 357
QY 371 TCCTCA 376
Db 358 TCCTCA 363

RESULT 5
LOCUS HSA279520 366 bp mRNA linear PRI 01-JUN-2000
DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial cds.
ACCESSION AJ279520
VERSION 1
KEYWORDS IGH; IgM heavy chain; immunoglobulin mu heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Chiorazzi, N. and Ferrarini, M.
TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents
JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)
MEDLINE 20281644
PUBMED 10820234
REFERENCE 2 (bases 1 to 366)
AUTHORS Dono, M.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="CD27low-8"
/cell_type="IgD-low SE B-lymphocyte"
/tissue_type="tonsil"
/rearranged
1..366
/gene="IGHV4-4"
/c1..>366
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/codon_start=1
/product="immunoglobulin mu heavy chain variable region"
/protein_id="CAB66350.1"
/db_xref="GI:6723538"
/db_xref="EMBL:U00000.1"
/translation="QVQLQESGPGLVKPSGTLSTLTCAVSGGSSSSNWNWSWVQPPGK GLEWIGIYHSGSTNYPNLSKRVITISVDKSKNQFSLKUSVTAADTAVTYCARDWAI GVVIMFGYWGQSTLVTVSS"
1..>366
/gene="IGHV4-4"
/product="immunoglobulin mu heavy chain variable region"

V_region
ORIGIN
Query Match 70.1%; Score 263.4; DB 9; Length 366;
Best local Similarity 85.9%; Pred. No. 6.6e-63;

Matches 317; Conservative 0; Mismatches 46; Indels 6; Gaps 2;
QY 11 CAGCTGAGCTGAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGAGAGACCCCTGTGTCCTC 70
Db 1 CAGGTGAGCTGAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGAGAGACCCCTGTGTCCTC 60
QY 71 ACCTGGCTGCTCTCTGGTGGCTCTGTGACAGTAGTAACTGTGTGACCTGATCCGCCAG 130
Db 61 ACCTGGCTGCTCTCTGGTGGCTCTGTGACAGTAGTAACTGTGTGACCTGATCCGCCAG 120
QY 131 CCCCCAGGGAAGGCACTGGAGTGGATTGACAGCTATCTCTGGTAGTGGGGCCACCAAC 190
Db 121 CCCCCAGGGAAGGCTGGAGTGGATTGAGAAATCTATCATA--GTGGAGCACCAAC 177
QY 191 TACAACCGTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACAGTCCTCAAGAACCAAGTTC 250
Db 178 TACAACCGTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACAGTCCTCAAGAACCAAGTTC 237
QY 251 TCCTGAACTGAACCTCTGTGACCGCGGACAGCCGCTGATTACTGTGTCACAGAT 310
Db 238 TCCTGAACTGAACCTCTGTGACCGCGGACAGCCGCTGATTACTGTGTCACAGAT 297
QY 311 TGGGCCCCAAAT---AGCTGGAACACGCTAGGCTTCTGGGCCCCAGGAGTCTTGTCACCC 367
Db 298 ATGGCGATTTTGGAGTGGTTATTATTTCCGGTACTGGGGCCAGGAAACCCCTGTGTCACC 357
QY 368 GTCTCTCA 376
Db 358 GTCTCTCA 366

RESULT 6
LOCUS HSU80180 368 bp DNA linear PRI 19-FEB-1997
DEFINITION Human immunoglobulin heavy chain variable region (V4-4b) gene, partial cds.
ACCESSION U80180
VERSION 1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 368)
AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.
TITLE Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE 97182739
PUBMED 9030878
REFERENCE 2 (bases 1 to 368)
AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="14"
/map="14q32-q33"
/clone="tt3a6"
/cell_type="CD19+ B cells"
/tissue_type="peripheral blood"
/note="CB19+ peripheral blood B cells obtained from a healthy subject; clone 105 in reference 1"
1..309
/gene="V4-4b"
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/gene="V4-4b"
/note="Ig VH4 heavy chain"
/codon_start=1

/product="immunoglobulin heavy chain variable region"
/protein_id="AAC51095.1"
/db_xref="GI:1791203"
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GLEWIGELVHSGSTYNPSLKSRTVTSVDKSNQPSLKSSTVAADTAATVAVYCARDEL
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ORIGIN

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QY 71 ACCTGCGCTGTCTCTGGTGGCTCTGTGACAGTAGTAACCTGTGAGACCTGGATCGCCAG 130
Db 61 ACCTGCGCTGTCTCTGGTGGCTCTGTGACAGTAGTAACCTGTGAGTGGTGGTGGTGGCAG 120

QY 131 CCCCAGGAGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 190
Db 121 CCCCAGGAGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 177

QY 191 TACAACCCGCTCCCTCAAGAGTCGAGTCACTATTCACAAGACACCTCCAAAGAACCCAGTTC 250
Db 178 TACAACCCGCTCCCTCAAGAGTCGAGTCACTATTCACAAGAACCCAGTTC 237

QY 251 TCCTGAACTGAATCTGTGACCGCGCGGACACGGCCGTATTAATCTGTCGAGAGAT 310
Db 238 TCCTGAACTGAATCTGTGACCGCGCGGACACGGCCGTATTAATCTGTCGAGAGAT 297

QY 311 TGG-----GCCCAATAGCTGGAACAACGCTAGGCTTCGGGGCCAGGAGTCCCTGGTCA 365
Db 298 AGGTATTTGTAGTAGTACCAAGTGCACAAATTGATCTGAGGAGTGGAGTGGAGTGGAGTGGAGT 357

QY 366 CGTGTCTCTCA 376
Db 358 CGTGTCTCTCA 368

RESULT 7

HSA245032 363 bp mRNA linear PRI 01-JUN-2000
LOCUS
DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone 1-F24.

ACCESSION AJ245032
VERSION J. Immunol. 164 (11), 5596-5604 (2000)
KEYWORDS Igm; Igm heavy chain; immunoglobulin mu heavy chain; variable region.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M.

TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

J. Immunol. 164 (11), 5596-5604 (2000)

JOURNAL

MEDLINE 20281644

PUBMED 10820234

REFERENCE

2 (bases 1 to 363)

Dono, M.

Direct Submission

Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova, ITALY

FEATURES

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Db 61 ACCTGCGCTGTCTCTGGTGGCTCTGTGACAGTAGTAACCTGTGAGTGGTGGTGGTGGCAG 120

QY 131 CCCCAGGAGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 190
Db 121 CCCCAGGAGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 177

QY 191 TACAACCCGCTCCCTCAAGAGTCGAGTCACTATTCACAAGACACCTCCAAAGAACCCAGTTC 250
Db 178 TACAACCCGCTCCCTCAAGAGTCGAGTCACTATTCACAAGAACCCAGTTC 237

QY 251 TCCTGAACTGAATCTGTGACCGCGCGGACACGGCCGTATTAATCTGTCGAGAGAT 310
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QY 311 TGGGCCCAATAGCTGGAACAACGCTAGGCTTCGGGGCCAGGAGTCCCTGGTCAACCGTTC 370
Db 298 GAGTATAGCAGCAGATTCACCTGTTGACCCCTGGGGCCAGGAGACCTGGTCAACCGTTC 357

QY 371 TCCTCA 376
Db 358 TCCTCA 363

RESULT 8

HSA279522

LOCUS

DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone CD2710w-12.

ACCESSION AJ279522

VERSION 1

KEYWORDS Igm; Igm heavy chain; immunoglobulin mu heavy chain; variable region.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M.

TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

J. Immunol. 164 (11), 5596-5604 (2000)
20281644
PUBMED 10820234
REFERENCE 2 (bases 1 to 363)
AUTHORS Dono, M.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY

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Db 1 CAGGTGAGTGTGAGAGTGGGCGCCAGAGTGTGAAGCTTCGGGAGACCTGTCCCTC 60
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Db 61 ACCTGCGCTCTCTGCTGCTCTGTCAGCAGTAGTAACCTGGTGGACCTGGATCCGCGAG 120
Qy 131 CCCCAGGAGGAGTGGAGTGGATTCCTGCTGATGTGGTGGGCGCCACCAAC 190
Db 121 CCCCAGGAGGAGTGGAGTGGATTCCTGCTGATGTGGTGGGCGCCACCAAC 177
Qy 191 TACAGCCGTCCTCCACAGATCGAGTGCATCTTTCACAGACAGCTCCAGACCACTTC 250
Db 178 TACAGCCGTCCTCCACAGATCGAGTGCATCTTTCACAGACAGCTCCAGACCACTTC 237
Qy 251 TCCCTGAACCTGAACCTCTGTACCGCGCGGACACCGCGCTGTATTAATCTGTGCGAGAT 310
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Best Local Similarity 83.1%; Pred. No. 1e-60;
Matches 304; Conservative 0; Mismatches 59; Indels 3; Gaps 1;
Qy 11 CAGTGTGAGTGTGAGAGTGGGCGCCAGAGTGTGAAGCTTCGGAGACCTGTCCCTC 70
Db 1 CAGGTGAGTGTGAGAGTGGGCGCCAGAGTGTGAAGCTTCGGGAGACCTGTCCCTC 60
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Db 61 ACCTGCGCTCTCTGCTGCTCTGTCAGCAGTAGTAACCTGGTGGACCTGGATCCGCGAG 120
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Db 121 CCCCAGGAGGAGTGGAGTGGATTCCTGCTGATGTGGTGGGCGCCACCAAC 177
Qy 191 TACAGCCGTCCTCCACAGATCGAGTGCATCTTTCACAGACAGCTCCAGACCACTTC 250
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Db 238 TCCCTGAACCTCTGTGACCGCGCGGACACCGCGCTGTATTAATCTGTGCGAGTAA 297

RESULT 9
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LOCUS HSA244946 363 bp mRNA linear PRI 01-JUN-2000
DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable

region, partial, clone 3-A1.
AJ244946
VERSION AJ244946.1 GI:4995351
KEYWORDS IGM; IGM heavy chain; immunoglobulin mu heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M.
TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents
JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)
MEDLINE 20281644
PUBMED 10820234
REFERENCE 2 (bases 1 to 363)
AUTHORS Dono, M.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY

FEATURES
source Location/Qualifiers
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Db 1 CAGGTGAGTGTGAGAGTGGGCGCCAGAGTGTGAAGCTTCGGGAGACCTGTCCCTC 60
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Db 121 CCCCAGGAGGAGTGGAGTGGATTCCTGCTGATGTGGTGGGCGCCACCAAC 177
Qy 191 TACAGCCGTCCTCCACAGATCGAGTGCATCTTTCACAGACAGCTCCAGACCACTTC 250
Db 178 TACAGCCGTCCTCCACAGATCGAGTGCATCTTTCACAGACAGCTCCAGACCACTTC 237
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QY 311 TGGGCCCAAAATAGCTGGAAACAACGCTAGGCTCTGGGGCCAGGAGTCTGGTCCACGCTC 370
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QY 371 TCCTCA 376
DB 358 TCCTCA 363

RESULT 10
HSA279549 363 bp DNA linear PRI 01-JUN-2000
LOCUS Homo sapiens DNA for immunoglobulin heavy chain variable region,
DEFINITION partial, clone IgM-only-16.
ACCESSION AJ279549
VERSION AJ279549.1 GI:6723593
KEYWORDS immunoglobulin heavy chain; variable region; VH4 family.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Dono, M., Zupo, S., Leanza, N., Melicci, G., Fogli, M., Melagrana, A.,
Chiorazzi, N., and Ferrarini, M.
TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
J. Immunol. 164 (11), 5596-5604 (2000)
JOURNAL 20281644
MEDLINE 10820234
PUBMED
REFERENCE 2 (bases 1 to 363)
AUTHORS Dono, M.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
ITALY

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DB 1 CAGGTGCAGCTCGAGAGTCGGCCCGAGAGTGGTGAAGCTTCGGAGACCTGTCCTCCCTC 60
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DB 61 ACCTGGCTGTCTCTGGTGGCTCCATCAGCAGTAGTAACCTGGTGGAGTTGGGTCCGCCAG 120
QY 131 CCCCCAGGGAAGGAGCTGGAGTGGATTTGGACGCTATCTCTGGTAGTGGTGGGCCACCAAC 190
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DB 178 TACAACCCGCTCCTCAAGAGTCGAGTCATCAATTTCAAGACACCTCCAGACCCAGTTC 237
QY 251 TCCTCGAACCTGAACCTCTGTGACCGCGCGGACACCGCCGCTGTATTACTGTGCCAGAGAT 310
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QY 371 TCCTCA 376
DB 358 TCCTCA 363

RESULT 11
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LOCUS Human immunoglobulin heavy chain variable region (V4-4b) gene,
DEFINITION partial cds.
ACCESSION U80141
VERSION U80141.1 GI:1791124
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 366)
AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.
TITLE Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient
J. Clin. Exp. Immunol. 107 (2), 372-380 (1997)
JOURNAL 903878
MEDLINE
PUBMED
REFERENCE 2 (bases 1 to 366)
AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.B.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA

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V_region
ORIGIN

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71  ACCTGCGCTCTCTGCTGGCTCTGTCAGCAGTGAATGGAAGCTTCTGCTGAGTGGGAGTCCGAC 130
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191 TACAAACCGCTCTCAAGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 250
Db 178 TACAAACCGCTCTCAAGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 237

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311 TGGGCCCCAAATAGCTGAA 364 bp DNA linear PRI 19-FEB-1997
LOCUS Human immunoglobulin heavy chain variable region (V4-4b) gene,
partial cds.
U80125
U80125.1 GI:1791092
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 364)
Glas.A.M., Nottenburg, C. and Milner, E.C.
Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient
Clin. Exp. Immunol. 107 (2), 372-380 (1997)
JOURNAL: 97182739
MEDLINE 9030878
PUBMED 9030878
REFERENCE 2 (bases 1 to 364)
Glas.A.M., Nottenburg, C. and Milner, E.C.B.
Direct Submission
AUTHORS Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
JOURNAL Location/Qualifiers
FEATURES
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Best Local Similarity 84.5%; Pred. No. 2.5e-60;
Matches 310; Conservative 0; Mismatches 53; Indels 4; Gaps 2;

11  CAGCTGACGCTGCAGGAGTGGGCCCCAGGAGTGGTGAAGCTTTCGAGACCTGTCCCTC 70
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71  ACTGCGCTCTCTGCTGGCTCTGTCAGCAGTGAATGGAAGCTTCTGCTGAGTGGGAGTCCGAC 130
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191 TACAAACCGCTCTCAAGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 250
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311 TGGGCCCCAAATAGCTGAA 364 bp mRNA linear PRI 30-JUL-1999
LOCUS Homo sapiens partial mRNA for immunoglobulin heavy chain variable
region (IGHV gene), sample GN08.
U80125
U80125.1 GI:5679481
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 375)
Gaidano, G., and Ferrarini, M.
Identification of three subgroups of B-cell chronic lymphocytic
leukemia bases upon mutations of BCL-6 and IGV genes
Unpublished
AUTHORS Fais, F.
JOURNAL Direct Submission
FEATURES
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ORIGIN

Query Match 57.6%; Score 254; DB 9; Length 375;
Best Local Similarity 84.7%; Pred. No. 2.8e-60;
Matches 310; Conservative 0; Mismatches 50; Indels 6; Gaps 2;
QY 11 CAGCTGCAGCTCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 70
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QY 191 TACACCCCTGCTCAAGAGTGCAGTGCATATTTCAAGAGACGTTCMAAGAACCAAGTTC 250
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QY 311 TGGGCCCAATAGCTGGAACACGCTAGCTTCTTGGGGCCAGGAGTCTGTGTCACCGTCT 370
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QY 371 TCCTCA 376
DB 355 TCCTCA 360

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AY376082
LOCUS
DEFINITION Homo sapiens isolate VH-CE-A54 immunoglobulin E heavy chain
variable region mRNA, partial cds.
ACCESSION AY376082
VERSION AY376082.1 GI:37014228
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Davies, J.M. and O'Hehir, R.E.
TITLE VH gene usage in IgE responses of grass pollen allergic individuals
is oligoclonal and antigen driven
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 364)
AUTHORS Davies, J.M. and O'Hehir, R.E.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-2003) Allergy, Immunology and Respiratory
Medicine, The Alfred Hospital, Commercial Road, Melbourne, VIC

3004, Australia
Location/Qualifiers
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ORIGIN

Query Match 67.3%; Score 253; DB 9; Length 364;
Best Local Similarity 82.7%; Pred. No. 5.4e-60;
Matches 302; Conservative 0; Mismatches 60; Indels 3; Gaps 1;
QY 12 AGCTGCAGCTCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 71
DB 2 AGGTGCAGCTGCTCGAGTTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 61
QY 72 CTTGGCTGTCTCTGGTGGCTCTGTACAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGC 131
DB 62 CTTGCAGCTGTCTCTGGTGGCTCTGTACAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGC 121
QY 132 CCCCAGGAGGAGGAGCTGAGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGCCCAACCACT 191
DB 122 CCCCAGGAGGAGGAGCTGAGAGTGGATTGGAGTAATCTATCATA---GTGGAGGACCTTCT 178
QY 192 ACAACCCCTGCTCAAGAGTGCAGTGCATATTTCAAGAGACGTTCMAAGAACCAAGTTC 251
DB 179 ACAACCCCTGCTCAAGAGTGCAGTGCATATTTCAAGAGACGTTCMAAGAACCAAGTTC 238
QY 252 CCCTGAACCTGAACCTGTCGACCGCCGCGGACACGCGGTGTATTACTGTGCCAGAGAT 311
DB 239 CCCTGAACCTGAGCTCTGTGACCGCCGCGGACACGCGGTGTATTACTGTGCCAGAGAT 298
QY 312 GGGGCCCAATAGCTGGAACACGCTAGCTTCTTGGGGCCAGGAGTCTGTGTCACCGTCT 371
DB 299 GGGAGAGCTACGCGGGGAGGAGTTTGACTACTTGGGGCCAGGAAACCTGTGTCACCGTCT 358
QY 372 CCTCA 376
DB 359 CCTCA 363

RESULT 15
HSA556684
LOCUS
DEFINITION Homo sapiens partial mRNA for immunoglobulin gamma heavy chain
variable region (IGHV4-04 gene), clone IA-4G 019.
ACCESSION AJ556684
VERSION AJ556684.1 GI:3137609
KEYWORDS IGHV4-04 gene; immunoglobulin gamma heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Colombo, M., Dono, M., Gazzola, P., Chiorazzi, N., Mancardi, G. and
Ferrarini, M.
TITLE Maintenance of B lymphocytes related clones in the cerebrosplinal
fluid of multiple sclerosis patients
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 363)
AUTHORS Colombo, M.
TITLE Direct Submission

JOURNAL Submitted (26-FEB-2003) Colombo M., Medical Oncology C. IST-IST.
Nazione. Ricerca Cancro. Largo Rosanna Benzi 10, Genova 16132, ITALY

FEATURES
source

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V_region

ORIGIN

Query Match 67.1%; Score 252.4; DB 9; Length 363;
Best Local Similarity 82.5%; Pred. No. 8e-60;
Matches 302; Conservative 0; Mismatches 61; Indels 3; Gaps 1;
Qy 11 CAGCTGACCTGCAGGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 70
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Db |||||
Qy 71 ACCTGCGCTGTCTCTGTGGCTCTGTCTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 130
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Qy 61 ACCTGCGCTGTCTCTGTGGCTCTGTCTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
Db |||||
Qy 131 CCCCAGGGAAGGACCTGGAGTGGATGGACGTATCTCTGTGTAGTGGTGGGCCACCAAC 190
Db |||||
Qy 121 CCCCAGGGAAGGACCTGGAGTGGATGGAGAAATCTATCATA---GTGGAGACCCAGG 177
Db |||||
Qy 191 TACAAACCGTCCCTCAAGAGTCGAGTCATCATTTCAAGACACGTCACAGAACCAAGTTC 250
Db |||||
Qy 178 TACAAACCGTCCCTCAAGAGTCGAGTCACATATCATAGTACAGTCCAGAACCAAGTTC 237
Db |||||
Qy 251 TCCCTGAACCTGAACCTGTGACCGCCGACACCGCGGTGATTAATCTGTGCCAGAGAT 310
Db |||||
Qy 238 TCCCTGAACCTGAACCTGTGACCGCCGACACCGCGGTGATTAATCTGTGCCAGAGAT 297
Db |||||
Qy 311 TGGGCCCAATAGCTGGAAACACGCTTCTGGGGCCAGGAGTCTGGTCCACCGTC 370
Db |||||
Qy 298 AGTTTCTATGATAGCGGGGGTGTCTTTTGTATCTGGGCCAAGGACAAATGGTCCCGTC 357
Db |||||
Qy 371 TCCTCA 376
Db |||||
Qy 358 TCTTCA 363

Search completed: June 19, 2004, 07:02:22
Job time : 1848 secs

CC an epitope in domain 5 of trkC. The antibodies of the invention are
CC effective in the treatment of cisplatin- or pyridoxine-induced
CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre
CC sensory neuropathy, neurodegenerative disease including amyotrophic
CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood
CC cells such as leukopenia including eosinopenia, basopenia,
CC lymphopenia, monocytopenia, neutropenia, Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and tumours. The sequences are
CC also useful for inducing angiogenesis for treating wounds, ulcers and
CC diabetic complications of sickle cell disease, for treating cardiac
CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases
CC involving cellular degeneration. Sequences ABK24399-ABK24413 represent
CC DNA molecules encoding human and mouse anti-trkC agonist monoclonal
CC antibodies and antibody fragments of the invention
XX
XX
SQ Sequence 354 BP; 73 A; 107 C; 103 G; 71 T; 0 U; 0 Other;
Query Match 64.7%; Score 243.2; DB 6; Length 354;
Best Local Similarity 85.0%; Pred. No. 1.6e-57;
Matches 311; Conservative 0; Mismatches 43; Indels 12; Gaps 3;
QY 11 CAGCTGCAGCTGCAGGAGTGGGGCCCGAGAGTGGTGAAGCTTCGGAGACCTTCCTCCTC 70
Db 1 CAGGTGCAGCTGCAGGAGTGGGGCCCGAGAGTGGTGAAGCTTCGGAGACCTTCCTCCTC 60
QY 71 ACCTGCGCTCTCTGTTGGCTCTCTCAGCAGTGTACTGTTGACCTGGATCGGCCAG 130
Db 61 ACCTGCATCTCTCTGTTGGCTCTCTCAGCAGTGTACTGTTGACCTGGATCGGCCAG 117
QY 131 CCCCAGGAGGAGCTGAGTGGATTTGAGCGTATCTCTGTTAGTGGTGGGGCCCGACCAAC 190
Db 118 CCGCGGAGGAGGAGCTGAGTGGATTTGAGCGTATCTCTGTTAGTGGTGGGGCCCGACCAAC 174
QY 191 TACAACCGCTCCCTCAAGAGTCGAGTCATCTTTCACAGACACGTCCTCAAGAACCAAGTTC 250
Db 175 TACAACCGCTCCCTCAAGAGTCGAGTCATCTTTCACAGACACGTCCTCAAGAACCAAGTTC 234
QY 251 TCCCTGAACCTGAACCTGTGACCGCCCGGACACGCGCGTGTATTACTGTGCGAGAGAT 310
Db 235 TCCCTGAACCTGAACCTGTGACCGCCCGGACACGCGCGTGTATTACTGTGCGAGAGAT 294
QY 311 TGGGCGCAATAGCTGGACACGCTAGGCTTCTTGGGGCCAGGAGTCTGTGTCACCGTC 370
Db 295 GGGGGCTACA-----GTAAACCTTTTACTACTGGGGCCAGGAACTTGTGTCACCGTC 348
QY 371 TCCTCA 376
Db 349 TCCTCA 354
RESULT 2
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ID AAT45035 standard; cDNA; 372 BP.
XX
AC AAT45035;
XX
DT 23-MAY-1997 (first entry)
XX
DE Human lung cancer specific antibody heavy chain variable region cDNA.
XX
KW Heavy chain; light chain; variable region; human; monoclonal antibody;
XX lung cancer tissue; diagnosis; purification; cancer-specific antigen; ss.
OS Homo sapiens.
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FT /note= "Fig 6, Claim 7"
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FT /product= "CDR3"
FT /note= "Fig 7, Claim 7"
XX
XX JP08280386-A.
XX 29-OCT-1996.
XX 14-APR-1995; 95JP-00112671.
XX 14-APR-1995; 95JP-00112671.
XX (MOMI) MORINAGA & CO LTD.
XX WPI: 1997-014849/02.
XX P-PSDB; AAW06474.
XX
XX Antibody specifically reactive to human lung cancer cells - also
XX corresponding DNA, used to diagnose cancer, or for purification of cancer
XX -specific antigen.
XX
XX Claim 1; Fig 1; 9pp; Japanese.
XX
XX The sequences given in AAT45035-36 encode the heavy chain and light chain
XX variable regions from a human monoclonal antibody which is specific for
XX human lung cancer tissue. The monoclonal antibody may be used for
XX clinical diagnosis of cancers, for immunological therapy or for
XX purification of a cancer-specific antigen
XX
XX Sequence 372 BP; 77 A; 102 C; 117 G; 76 T; 0 U; 0 Other;
Query Match 64.6%; Score 243; DB 2; Length 372;
Best Local Similarity 82.1%; Pred. No. 1.8e-57;
Matches 308; Conservative 0; Mismatches 55; Indels 12; Gaps 2;
QY 11 CAGCTGCAGCTGCAGGAGTGGGGCCCGAGAGTGGTGAAGCTTCGGAGACCTTCCTCCTC 70
Db 1 CAGGTGCAGCTGCAGGAGTGGGGCCCGAGAGTGGTGAAGCTTCGGAGACCTTCCTCCTC 60
QY 71 ACCTGCGCTCTCTGTTGGCTCTCTCAGCAGTGTACTGTTGACCTGGATCGGCCAG 130
Db 61 ACCTGCGCTCTCTGTTGGCTCTCTCAGCAGTGTACTGTTGACCTGGATCGGCCAG 120
QY 131 CCCCAGGAGGAGCTGAGTGGATTTGAGCGTATCTCTGTTAGTGGTGGGGCCCGACCAAC 190
Db 121 CCCCAGGAGGAGGAGCTGAGTGGATTTGAGCGTATCTCTGTTAGTGGTGGGGCCCGACCAAC 177
QY 191 TACAACCGCTCCCTCAAGAGTCGAGTCATCTTTCACAGACACGTCCTCAAGAACCAAGTTC 250
Db 178 TACAACCGCTCCCTCAAGAGTCGAGTCATCTTTCACAGACACGTCCTCAAGAACCAAGTTC 237
QY 251 TCCCTGAACCTGAACCTGTGACCGCCCGGACACGCGCGTGTATTACTGTGCGAGAG 307
Db 238 TCCCTGAAGGTGAACCTGTGTCACCGCCCGGACACGCGCGTGTATTACTGTGCGAGAG 297
QY 308 -----GATTGGGGCCCAATAGCTGGAACAACAGCTAGGCTTCTGCGGGCCAGGAGTCTG 361
Db 298 AATTACGATTTTGGAGTGGTGGCGAGCGGCCCATTTGACTACTGGGGCCAGGAGCGCTG 357
QY 362 GTCACCGTCTCTCA 376
Db 358 GTCACCGTCTCTCA 372
RESULT 3
ABS57441
ID ABS57441 standard; cDNA; 360 BP.
XX

ABS57441;
20-FEB-2003 (first entry)
Human monoclonal antibody Fl.1 heavy chain variable region cDNA.
Human; monoclonal antibody; Fl.1; Mab Fl.1; heavy chain variable region;
gene; ss; antigen-binding protein; alpha3(IV) NCI collagen;
anti-GBM disease; anti-glomerular basement membrane autoantibody disease;
immunosuppressive.
Homo sapiens.
Key Location/Qualifiers
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FT /product= "Human Mab Fl.1 heavy chain variable region"
FT /partial
FT /note= "No start or stop codon shown"
WO200285924-A2.
31-OCT-2002.
23-APR-2002; 2002WO-US013063.
23-APR-2001; 2001US-0285860P.
(ABGE-) ABGENIX INC.
(UYPE-) UNIV PENNSYLVANIA.
Madaio MP, Gallo ML;
WPI: 2003-093089/08.
P-PSDB; ABG71454.
New human monoclonal antibody or its antigen-binding protein that
specifically binds alpha 3(IV) NCI collagen, useful for preparing
compositions for treating or preventing anti-glomerular basement membrane
disease.
Claim 13; Page 61; 80pp; English.
The invention relates to a human monoclonal antibody or its antigen-
binding protein which specifically binds alpha3(IV) NCI collagen and a
hybridoma cell line that produces the Fl.1 monoclonal antibody. The human
monoclonal antibody or its antigen-binding protein that specifically
binds alpha3(IV) NCI collagen is useful for preparing compositions for
treating or preventing human anti-glomerular basement membrane
autoantibody disease (anti-GBM disease). The sequences can also be used
for producing a mouse model for anti-GBM disease, for inducing anti-GBM
disease in a mouse and for screening or identifying compositions for
treating or preventing one or more symptoms of anti-GBM disease. This
sequence represents cDNA encoding a human monoclonal antibody Fl.1 (Mab
Fl.1) heavy chain variable region
Sequence 360 BP; 73 A; 110 C; 101 G; 76 T; 0 U; 0 Other;

Query Match 64.6%; Score 242.8; DB 7; Length 360;
Best Local Similarity 82.8%; Pred. No. 2.1e-57;
Matches 303; Conservative 0; Mismatches 57; Indels 6; Gaps 2;
QY 11 CAGCTGCAGCTGCAGGAGTCGGGCCAGAGTGTGAAGCTTTCGGAGACCTGTCCCTC 70
DB 1 CAGGTGCAGCTGCCTGAGTCGGGCCAGGAGTGTGAAGCTTTCGGGACCTGTCTCTC 60
QY 71 ACCTGCGCTGTCTGCTGCTGTCTGCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTG 130
DB 61 ACCGTGACATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 131 CCCCGAGGAGGAGGAGTGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 190
DB 121 TCCCGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 177
QY 191 TACAACCGCTCCCTCAAGAGTCGAGTCATCTTCAAGACACGTCACAGAACCGATTC 250
DB 178 TACAACCGCTCCCTCAAGAGTCGAGTCATCTTCAAGACACGTCACAGAACCGATTC 237
QY 251 TCCCTGAACCTGAACCTGTGACCCGCGGACACCGCGGTGTATTAATGTGCGCAGAGAT 310
DB 238 TCCCTGAAGATGACCTGTGACCCGCGGACACCGCGGTGTATTAATGTGCGCAGAGAT 294
QY 311 TGGGCCCAATAGCTGGAACCAACGCTAGGCTTCTGGGGCCACAGGAGTCTCTGTCACCGTC 370
DB 295 GCGGCCCAATAGCTGGAACCAACGCTAGGCTTCTGGGGCCACAGGAGTCTCTGTCACCGTC 354
QY 371 TCCTCA 376
DB 355 TCCTCA 360
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ABA94218
ID ABA94218 standard; DNA; 363 BP.
XX ABA94218;
XX 13-MAR-2002 (first entry)
XX ebvHGM MSI19D10 heavy chain variable region nucleotide sequence.
XX Neuromodulatory; central nervous system; CNS; SHIGM22; IYM 22; AKJR4;
XX ebvHGM MSI19D10; ebv HGM CB2bG8; CB2IE12; CB2IE7; MSI19B5; virucide;
XX antiparkinsonian; neuroprotective; nootropic; vulnerary; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..363
XX /*tag= a
XX WO200185797-A1.
XX 15-NOV-2001.
XX 30-MAY-2000; 2000NO-US014902.
XX 10-MAY-2000; 2000US-00568351.
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX Rodriguez M, Miller DJ, Pease LR;
XX WPI; 2002-066536/09.
XX P-PSDB; ABB07171.
XX Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
XX neurite outgrowth, regeneration, remyelination and neuroprotection in
XX central nervous system, useful to treat post-infectious
XX encephalomyelitis.
XX Claim 43; Fig 19; 219pp; English.
XX The invention provides a neuromodulatory agent (I) capable of promoting
XX neurite outgrowth, regeneration, remyelination and neuroprotection in
XX central nervous system (CNS). (I) is capable of inducing remyelination,
XX promoting cellular proliferation of glial cells, and promoting Ca2+
XX signaling with oligodendrocytes. An humanised antibody to (I) can be
XX selected from antibody SHIGM22 (LYM 22), ebvHGM MSI19D10, ebv HGM
XX CB2bG8, AKJR4, CB2IE12, CB2IE7 or MSI19B5. (I) is useful for stimulating
XX remyelination of CNS axons, stimulating proliferation of glial cells in
XX CNS axons, or treating demyelinating disease of CNS in a mammal in need
XX of such therapy. (I) is capable of binding to structures and cells within
XX CNS. (I) is preferably useful for treating a demyelinating disease of CNS
XX of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
XX (TMEV) or for treating a human being having multiple sclerosis, or a

KW Multiple sclerosis; cerebrospinal fluid; CSF; B-cell;
KW heavy chain variable region; VH gene; somatic hypermutation;
KW B-cell clonality; ML gene; diagnosis; human; ss.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
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XX W09915696-A1.
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XX 01-APR-1999.
XX
XX 17-SEP-1998;
XX 19-SEP-1997;
XX 04-NOV-1997;
PR 98WO-CAD000873.
PR 97CA-02216595.
PR 97CA-02220245.

XX (QINY/) QIN Y.
XX QIN Y;
XX WPI; 1999-276985/23.
XX P-PSDB; AAY05693.
XX
XX Determination of B-cell clonality by amplification or enzymatic
XX digestion.
XX
XX Disclosure; Fig 9B; 67pp; English.
XX
XX This is the nucleotide sequence of the heavy chain variable region (VH)
XX gene from a dominant clone, termed 4d68, of B-cells taken from the
XX cerebrospinal fluid (CSF) of a multiple sclerosis (MS) patient. Sequences
XX of VH of CSF B-cells were obtained from 4 MS patients (see AAY25316-19).
XX Differences in nucleotide and predicted amino acid (see AAY05691-94)
XX sequences were compared with the closest known germline VH genes; for
XX 4d68, this was ML. The results provided direct evidence that intrathecal
XX clonally expanded B-cells from the CSF of MS patients are hypermutated
XX postgerminal centre antibody-forming or memory lymphocytes that have
XX undergone antigen selection. This finding implicates an important
XX pathogenic pathway for the development of demyelination in CNS of MS. The
XX CC invention provides assay kits for determining B-cell or T-cell clonality.
XX CC This technology allows the establishment of clonal specific RNA library
XX CC from pathologic cells in the CNS of patients, which is important for
XX CC further understanding of the role of antigen(s) in the cause of B-cell
XX CC clonal expansion, and towards developing antigen specific therapeutic
XX CC strategy
XX
XX SQ Sequence 294 BP; 62 A; 84 C; 91 G; 57 T; 0 U; 0 Other;
XX
XX Query Match 64.1%; Score 241; DB 2; Length 294;
XX Best Local Similarity 90.6%; Pred. No. 6.2e-57;
XX Matches 269; Conservative 0; Mismatches 25; Indels 3; Gaps 1;
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XX QY 11 CAGCTGCAGCTGCAGAGTGGGCCCCAGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 70
XX DB 1 CAGGTGCAGCTGCAGAGTGGGCCCCAGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 60
XX
XX QY 71 ACCTGGCGTCTCTCTGGTGGCTCTGTTCAGCAGTAGTAACCTGGTGGACCTCGATCCGCGAG 130
XX DB 61 ACCTGGCGTCTCTCTGGTGGCTTCATCAGCAGTAGTAACCTGGTGGAGTTGGTCCGCGAG 120
XX
XX QY 131 CCCCCAGGAGGAGTGGAGTGGATTCAGTATCTCTGGTAGTGGTGGGCGACCAAC 190
XX DB 121 CCCCCAGGAGGAGTGGAGTGGATTCAGTATCTCTGGTAGTGGTGGGCGACCAAC 177
XX
XX QY 191 TACAACCCGTCCTCAAGAGTGGAGTCATCATTTCAAGACACGTCCTCAAGAACCAAGTTC 250
XX DB 178 TACAACCCGTCCTCAAGAGTGGAGTCATCATTTCAAGACACGTCCTCAAGAACCAAGTTC 237
XX
XX QY 251 TCCTTGAACCTGAACCTCTGTGACCCGCGGAGCACGGCCGCTGTATTACTGTGCCAGA 307
XX DB 238 TCCTTGAACCTGAACCTCTGTGACCCGCGGAGCACGGCCGCTGTATTACTGTGCCAGA 294
XX
XX
XX RESULT 7
XX ABS62723
XX ID ABS62723 standard; DNA; 358 BP.
XX
XX AC ABS62723;
XX
XX DT 24-OCT-2002 (first entry)
XX
XX DE Anti-IGF-IR antibody VH chain DNA consensus sequence #2.
XX
XX Insulin-like growth factor I receptor; antibody; human; ds; gene;
XX cytostatic; osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR;
XX tumour; anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy;
XX osteoporosis; acromegaly; gigantism; psoriasis; atherosclerosis.
XX

OS Homo sapiens.
 XX WO200253596-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-US051113.
 XX 05-JAN-2001; 2001US-0259927P.
 XX (PTIZ) PFIZER INC.
 XX (ABGE-) ABGENIX INC.
 XX Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
 XX WPI; 2002-575410/61.
 XX Novel humanized, chimeric monoclonal antibody that specifically binds to
 XX insulin-like growth factor I (IGF-I) receptor useful for inhibiting
 XX binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
 XX Disclosure; Fig 23; 172pp; English.
 XX This invention relates to a novel humanised, chimeric or human monoclonal
 XX antibody or its antigen binding portion that specifically binds to
 XX insulin-like growth factor I receptor (IGF-IR). The antibodies of the
 XX invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
 XX IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
 XX phosphorylation. The antibodies of the invention are useful for
 XX diagnosing the presence or location of an IGF-IR-expressing tumour in a
 XX subject. The antibody or its antigen-binding portion is also useful for
 XX treating cancer in a human. The method for this further involves an anti
 XX neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The
 XX antibodies may also be useful for increasing IGF-IR activity and thus
 XX restoring IGF-IR activity in a condition characterised by low IGF-IR
 XX levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
 XX also useful for inducing apoptosis of specific cells in a patient, and to
 XX treat non-cancerous states or disease, e.g. acromegaly, gigantism,
 XX psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
 XX minimise the immunogenic and allergic responses intrinsic to mouse or
 XX mouse-derived monoclonal antibodies and thus increase the efficacy
 XX and safety of the administered antibodies. The present sequence
 XX represents a DNA sequence encoding an anti-insulin-like growth factor I
 XX receptor antibody of the invention
 XX
 XX Sequence 358 BP; 70 A; 103 C; 101 G; 79 T; 0 U; 5 Other;
 XX
 XX Query Match 62.6%; Score 235.4; DB 6; Length 358;
 XX Best Local Similarity 82.5%; Pred. No. 2.3e-55;
 XX Matches 302; Conservative 4; Mismatches 51; Indels 9; Gaps 3;
 QY 11 CAGCTGCAGCTGCAGGAGTCCGCGCCAGAGTGTGAAGCCTTCGGAGACCCCTGTCCCTC 70
 DB 1 CAGGTGCAGCTGCAGGAGTCCGCGCCAGAGTGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
 QY 71 ACCTGCGCTGTCTCTGGTGGCTCTGTCTCAGCAGTGTGAAGTGTGATCGGACCTGGATCCGCGAG 130
 DB 61 ACCTGCAGCTGTCTCTGGTGGCTC---CATCAGTATTTACTGAGCTGTGATCCGCGAG 117
 QY 131 CCCCAGGAGGAGGAGCTGAGTGTGAAGTGTGAGTGTGATGTGTGGGGCCACCAAC 190
 DB 118 CCGCGCGGGAAGGAGCTGAGTGTGATGTGGGGCTATCT---ATACAGTGGAGGAGGAGGAG 174
 QY 191 TACAAACCGTCCCTCAAGAGTGTGATCATATTTCAAGACAGCTCCAGAACCACTTC 250
 DB 175 TACAAACCGTCCCTCAAGAGTGTGATCATATTTCAAGACAGCTCCAGAACCACTTC 234
 QY 251 TCCCTGAACTGAACTGTGACCGCCGCGACACCGCGGTGTATTTACTGTGCGAGAT 310
 DB 235 TCCCTGAACTGAACTGTGACCGCCGCGACACCGCGGTGTATTTACTGTGCG---GATA 291
 QY 311 TGGGCCCAATAGCTGGACACAGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCACCGTC 370

Db 292 ACCATTTTGGAGTGGTTATTATCTTGTACTGCGGCGCAGGANCCTGTCCGTC 351
 QY 371 TCCTCA 376
 DB 352 TCCTCA 357
 RESULT 8
 ABS20941
 ID ABS20941 standard; DNA; 362 BP.
 XX AC ABS20941;
 XX AC ABS20941;
 DT 19-AUG-2002 (first entry)
 XX Human genome-derived single exon probe ORF from lung SEQ ID NO 20932.
 XX Human; db; single exon probe; asthma; lung cancer; COPD; ILD;
 XX chronic obstructive pulmonary disease; interstitial lung disease;
 XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
 XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 XX primary ciliary dyskinesia; pulmonary hypertension;
 XX hyaline membrane disease; open reading frame; ORF.
 OS Homo sapiens.
 XX WO200186003-A2.
 XX 15-NOV-2001.
 XX 30-JAN-2001; 2001WO-US000665.
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX (MOLR-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 XX measure gene expression in human lung samples.
 PS Claim 4; SEQ ID NO 20932; 634pp; English.

The invention relates to a spatially-addressable set of single exon
 nucleic acid probes for measuring gene expression in a sample derived
 from human lung comprising single exon nucleic acid probes having one of
 12614 nucleic acid sequences mentioned in the specification, or their
 complements or the 12387 open reading frames derived from the 12614
 probes. Also included are a microarray comprising the novel set of probes
 ; the novel set of probes which hybridise at high stringency to a nucleic
 acid expressed in the human lung; measuring gene expression in a sample
 derived from human lung, comprising (a) contacting the array with a
 collection of detectably labeled nucleic acids derived from human lung
 mRNA, and (b) measuring the label detectably bound to each probe of the
 array; identifying exons in a eukaryotic genome, comprising (a)
 algorithmically predicting at least one exon from genomic sequences of
 the eukaryote; and (b) detecting specific hybridisation of detectably
 labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 having a fragment identical to the predicted exon, the probe is included
 in the above mentioned microarray; assigning exons to a single gene,
 comprising (a) identifying exons from genomic sequence by the method
 above and (b) measuring the expression of each of the exons in several

CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a single exon probe open reading frame of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 362 BP; 79 A; 103 C; 109 G; 71 T; 0 U; 0 Other;

Query Match 52.6%; Score 235.2; DB 6; Length 362;
Best Local Similarity 89.1%; Pred. No. 2.6e-55;
Matches 278; Conservative 0; Mismatches 28; Indels 6; Gaps 2;
QY 1 GGTCTGTCTCCAGCTGCGAGCTGCGAGAGTCGGGGCCAGAGTGGTGAAGCCTTCGGAGAC 60
DB 2 GGTCTGTCTCCAGCTGCGAGCTGCGAGAGTCGGGGCCAGAGCTGGTGAAGCCTTCGGAGAC 61
QY 61 CTGTCTCTCAGCTGGCTGTCTGTGGTGGTCTCTCAGCAGTAGTA---ACTGGTGGAC 117
DB 62 CTGTCTCTCAGCTGGCTGTCTGTGGTGGTCTCTCAGCAGTAGTA---ACTGGTGGAC 121
QY 118 CTGGATCGCCAGCCCCAGGAGAGGAGCTGGAGTGGAGTGGAGTATCTCTGGTAGTGG 177
DB 122 CTGGATCGCCAGCCCCAGGAGAGGAGCTGGAGTGGAGTGGAGTATCTATTA---G 178
QY 178 TGGGCGCCAGCACTACAACTCAACCCCTCCCTCAAGAGTGGAGTATCAATTCACAGACACGTC 237
DB 179 TGGGAGCACTACTACAACTCAACCCCTCCCTCAAGAGTGGAGTATCAATTCACAGACACGTC 238
QY 238 CAAGAACCACTTCTCCCTGAACTGACTCTGTGACCGCCGGACAGCGCGGTGATTA 297
DB 239 CAAGAACCACTTCTCCCTGAACTGACTCTGTGACCGCCGGACAGCGCGGTGATTA 298
QY 298 CTGTGCGCAGAGA 309
DB 299 CTGTGCGCAGACA 310

RESULT 9
ADE28490
ID ADE28490 standard; cDNA; 364 BP.
XX
AC ADE28490;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human anti-CD40 antibody 23-28-1H-D16E mutant VL heavy chain cDNA.
XX
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW human; light chain; ss; gene; mutant; 23-28-1H-D16E.
XX
OS Homo sapiens.
XX
XX
FN WO2003040170-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036107.

XX 09-NOV-2001; 2001US-0348980P.
PR (PFIZ) PFIZER PROD INC.
XX (ABGE-) ABGENIX INC.
PA
XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
PI
XX WPI; 2003-441521/41.
XX P-PSDB; ADE28491.
DR
XX New chimeric or human monoclonal antibody or its antigen-binding portion
XX that specifically binds to and activates human CD40, useful for enhancing
XX an immune response in a human, or treating cancer, HIV, neutropenia or
XX viral infections.
PS Claim 24; SEQ ID NO 97; 177pp; English.
XX
XX The invention relates to a novel chimeric or human monoclonal antibody or
XX its antigen-binding portion that specifically binds to and activates
XX human CD40. The anti-CD40 antibody of the invention demonstrates
XX cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
XX activities and may be useful for treating a hyperproliferative disorder
XX such as cancer, viral and bacterial infection or genetic, primary or
XX combined immunodeficiency conditions including neutropenia or HIV
XX infection. The anti-CD40 antibodies may also be useful for detecting CD40
XX in a biological sample in vitro or in vivo, as well as during gene
XX therapy procedures. The current sequence is that of the human anti-CD40
XX antibody mutant variable region heavy chain cDNA of the invention.

SQ Sequence 364 BP; 74 A; 108 C; 108 G; 74 T; 0 U; 0 Other;
Query Match 62.4%; Score 234.6; DB 9; Length 364;
Best Local Similarity 82.9%; Pred. No. 3.9e-55;
Matches 306; Conservative 0; Mismatches 54; Indels 9; Gaps 3;
QY 11 CAGCTGAGCTGCGAGAGTCGGGGCCAGAGTGGTGAAGCCTTCGGAGACCTTCCTC 70
DB 1 CAGCTGAGCTGCGAGAGTCGGGGCCAGAGTGGTGAAGCCTTCGGAGACCTTCCTC 60
QY 71 ACCTGCGCTGTCTCTGTGGTCTCTGTGAGCAGTAGTAACCTGTGGAGCTGGATCCGCGAG 130
DB 61 ACCTGCGCTGTCTCTGTGGTCTCTGTGAGCAGTAGTAACCTGTGGAGCTGGATCCGCGAG 117
QY 131 CCCCAGGAGAGGAGCTGGAGTGGAGTGGAGTATCTCTGTGGTGGTGGGCGCCAGCAAC 190
DB 118 CCCCCTGGGAGGAGCTGGAGTGGAGTGGAGTATCTATTA---GTGGAGACCAAC 174
QY 191 TACAACCCGCTCCCTCAGAGTGGAGTGGAGTATCTATTA---GTGGAGACCAAC 250
DB 175 TACAACCCGCTCCCTCAGAGTGGAGTGGAGTATCTATTA---GTGGAGACCAAC 234
QY 251 TCCCTGAACCTGAACTCTGTGACCGCGCGCGAGACAGCGCCGTGTATTA---GTGGAGAGAT 310
DB 235 TCCCTGAACCTGAACTCTGTGACCGCGCGCGAGACAGCGCCGTGTATTA---GTGGAGAGAT 294
QY 311 TGGGCGCCAAATAGCTG---GAACAACCGCTAGGCTTCGGGGCCAGGAGTCCCTGGTCAAC 367
DB 295 GGGGGCGCTTACCGGTGACTACGGCTGGTTCGCCCCCTGGGGCCAGGAGACCTTCGTCAAC 354
QY 368 GTCTCTCTCA 376
DB 355 GTCTCTCTCA 363

RESULT 10
AAQ33035
ID AAQ33035 standard; cDNA; 366 BP.
XX
AC AAQ33035;
XX
XX
DT 25-MAR-2003 (revised)
DT 06-MAY-1993 (first entry)

XX DE MAB 1-3-1 variable region of heavy chain.
XX KW Monoclonal antibody; hybridoma; PCR; variable region; constant region;
XX KW heavy chain; light chain; ss.
XX OS Synthetic.
XX PN EP520499-A1.
XX PD 30-DEC-1992.
XX PF 26-JUN-1992; 92EP-00110841.
XX PR 28-JUN-1991; 91JP-00158859.
XX PR 28-JUN-1991; 91JP-00158860.
XX PR 28-JUN-1991; 91JP-00158861.
XX PA (MITU) MITSUBISHI KASEI CORP.
XX PI Hosokawa S, Tagawa T, Hirakawa Y, Ito N, Nagaike K;
XX WPI; 1993-001328/01.
XX DR P-PSDB; AAR30145.
XX KW Human monoclonal antibody specific for a cancer cell membrane surface
XX PT antigen - prep'd. from a hybridoma obtd. by cell fusion between human
XX PS lymphocytes derived from cancer patients and mouse myeloma cells.
XX PS Claim 17; Page 31 + 18; 37pp; English.
XX CC A human MAB specifically binding to a surface antigen of cancer cell
XX CC membrane comprises variable regions of the heavy and light chains having
XX CC the amino acid sequences of AAR30145-46 respectively, encoded by DNA
XX CC sequences AAQ3035-36 respectively. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 366 BP; 76 A; 105 C; 111 G; 74 T; 0 U; 0 Other;

Query Match 62.4%; Score 234.6; DB 2; Length 366;
Best Local Similarity 81.0%; Pred. No. 3.9e-55;
Matches 299; Conservative 0; Mismatches 64; Indels 6; Gaps 2;
QY 11 CAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGAGACCTGTCCTCC 70
DB 1 CAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGAGACCTGTCCTCC 60
QY 71 ACTTGCGCTCTCTGCTGCTCTGTCAGCAGTAGTA---ACTGTGGACCTGGATCCGC 127
DB 61 ACTTGCACTCTCTGCTGCTCTGTCATCAGCAGTAGTAGTTACTTACTTGGGCTGGATCC 120
QY 128 CAGCCCCAGGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 187
DB 121 CAGCCCCAGGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 177
QY 188 AACTACAACCCCTCCCTCAGAGTGCAGTCAATTTCAAGACACGTCACGTCACGTCAC 247
DB 178 TACTACAACCCCTCCCTCAGAGTGCAGTCAATTTCAAGACACGTCACGTCACGTCAC 237
QY 248 TTCTCCCTGAACTGAACTGTAAGTGGGCGCGGAGACAGCCGCTGTTACTGTGCGACA 307
DB 238 TTCTCCCTGAACTGAACTGTAAGTGGGCGCGGAGACAGCCGCTGTTACTGTGCGAGG 297
QY 308 GATTGGGCGGCAATAGCTGGAACAAGCTAGGCTTCTGGGCGCGGAGGAGTCTGGTCC 367
DB 298 GGGAGCTACGGGGGCTACTACTAGGATGAGAGTCTGGGCGCGGAGGAGGAGGAGG 357
QY 368 GTCTCTCA 376
DB 358 GTCTCTCA 366

RESULT 11

AAZ49608/c
ID AAZ49608 standard; DNA; 351 BP.
XX AC AAZ49608;
XX DT 07-APR-2000 (first entry)
XX DE DNA-1 related to human antibody clone NHS76.
XX KW Human antibody clone NHS76; cytostatic; malignant tumour;
XX KW human histone H1; antibody; intracellular antigen; diagnosis; treatment;
XX KW tumour; cervical; ovarian; prostate; lung; liver; pancreatic; colon;
XX KW stomach; ds.
XX OS Homo sapiens.
XX PN WO200001822-A1.
XX PD 13-JAN-2000.
XX PF 02-JUL-1999; 99WO-GB002123.
XX PR 02-JUL-1998; 98GB-00014383.
XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Williams AJ, Tempest PR, Holtet TL, Jackson H;
XX WPI; 2000-137204/12.
XX PT New specific binding members capable of binding an intracellular antigen,
XX PT useful in the treatment and diagnosis of tumors.
XX PS Disclosure; Page 64; 70pp; English.
XX CC The present DNA sequence is related to human antibody clone NHS76. NHS76
XX CC is useful for targeting the necrotic centres of malignant tumours by
XX CC binding to human histone H1 and other intracellular antigens. The
XX CC specific binding members based on the CDRs (complementarity determining
XX CC regions) of NHS76 can be used in diagnosis and treatment of tumours like
XX CC cervical, ovarian, prostate, lung, liver, pancreatic, colon and stomach
XX CC tumours. Note: There is no relevant information regarding this sequence
XX CC in the specification
XX SQ Sequence 351 BP; 75 A; 103 C; 99 G; 74 T; 0 U; 0 Other;

Query Match 62.3%; Score 234.4; DB 3; Length 351;
Best Local Similarity 82.0%; Pred. No. 4.4e-55;
Matches 300; Conservative 0; Mismatches 51; Indels 15; Gaps 2;
QY 11 CAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGAGACCTGTCCTCC 70
DB 351 CAGGTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGAGACCTGTCCTCC 292
QY 71 ACCTGCGCTGCTCTGCTGCTGCTCTGTCAGCAGTAGTAACCTGGTGGACCTGGATCCG 130
DB 291 ACCTGCGCTGCTCTGCTGCTGCTTACTCCATCAGCAGTGGTTACTACTGGGCTGGATCCG 232
QY 131 CCCCAGGAGGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 190
DB 231 CCCCAGGAGGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 175
QY 191 TACAACCCGCTCCCTCAAGAGTGCAGTCAATTTCAAGACACGTCACGTCACGTCACG 250
DB 174 TACAACCCGCTCCCTCAAGAGTGCAGTCAATTTCAAGACACGTCACGTCACGTCACG 115
QY 251 TCCCTGAACTGAACTGTAAGTGGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 310
DB 114 TCCCTGAACTGAACTGTAAGTGGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 55
QY 311 TGGGCGGCAAAATAGCTGGAACAACGCTAGGCTTCTGGGCGCGGAGGAGGAGGAGGAGG 370
DB 54 AAG-----TGGTCCAGAGTTTGGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7


```
QY 371 TCCTCA 376
Db 6 TCTTCA 1

RESULT 12
AAZ49590
ID AAZ49590 standard; DNA; 351 BP.
XX
XX
AC AAZ49590;
XX
XX 07-APR-2000 (first entry)
XX
XX Human antibody clone NHS76 VH gene.
DE
XX Human antibody clone NHS76 VH; VH; heavy chain variable region;
XX cytostatic; malignant tumour; human histone H1; antibody;
XX intracellular antigen; diagnosis; treatment; tumour; cervical; ovarian;
XX prostate; lung; liver; pancreatic; colon; stomach; prodrug; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1. 351
CDS
FT /*tag= a
FT /product= "Human antibody clone NHS76 VH"
FT /note= "no stop codon given"
XX
XX WO200001822-A1.
XX
XX 13-JAN-2000.
XX
XX 02-JUL-1999; 99WO-GB002123.
XX
XX 02-JUL-1999; 98GB-00014383.
XX
XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Williams AJ, Tempest PR, Holtet TL, Jackson H;
XX
XX WPI; 2000-137204/12.
XX
XX P-PSDB; AAY44615.
XX
XX New specific binding members capable of binding an intracellular antigen,
XX useful in the treatment and diagnosis of tumors.
XX
XX Claim 15; Fig 1; 70pp; English.
XX
XX The present sequence encodes human antibody clone NHS76 heavy chain
XX variable region. This is useful for targeting the necrotic centres of
XX malignant tumours by binding to human histone H1 and other intracellular
XX antigens. The NHS76 VH gene can be used in the construction of expression
XX vectors. The specific binding members based on the CDRs (complementarity
XX determining regions) of NHS76 can be used in diagnosis and treatment of
XX tumours like cervical, ovarian, prostate, lung, liver, pancreatic, colon
XX and stomach tumours. The antibody is labelled with functional labels such
XX as toxins and enzymes which are capable of converting prodrugs into
XX active drugs at the site of a tumour
XX
XX Sequence 351 BP; 74 A; 99 C; 103 G; 75 T; 0 U; 0 Other;

Query Match 62.3%; Score 234.4; DB 3; Length 351;
Best Local Similarity 82.0%; Pred. No. 4.4e-55;
Matches 300; Conservative 0; Mismatches 51; Indels 15; Gaps 2;

QY 11 CAGCTGCAGCTGCAGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTGCTC 70
Db 1 CAGGTGCAGCTGCAGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTGCTC 60
QY 71 ACCTCGCTGTCTGTGGCTCTGTAGAGTACTGTGAGCTGGATCCGCGAG 130
Db 61 ACCTCGCTGTCTGTGGCTCTGTAGAGTACTGTGAGCTGGATCCGCGAG 120

131 CCCCAGGAGGAGGACTGGAGTGGAGTGGAGTATCTCTGTAGTGGTGGGGCCACCAAC 190
121 CCCCAGGAGGAGGAGTGGAGTGGAGTGGAGTATCTATCATA---GTGGAGCACCTAC 177
191 TACAACCCGTCCTCAAGAGTCGAGTCATCATTTCAACAGACAGCTCCAGAACACCTTC 250
178 TACAACCCGTCCTCAAGAGTCGAGTCATCATTTCAACAGACAGCTCCAGAACACCTTC 237
251 TCCCTGAACCTGAACTCTGTGACCGCGCGGACACCGCCCTGTATTACTGTGCCAGAGAT 310
238 TCCCTGAAGCTGAGCTCTGTGACCGCGCGGACACCGCCCTGTATTACTGTGCCAGAGGG 297
311 TGGGCCCAATAGCTGGAACAACGCTAGGCTTCTGGGGGCCAGGAGTCTGGTCAACGTC 370
298 AAG-----TGGTGAAGTTTGACTATTGGGGGCCAAGGCACCTCTGTCACCGTC 345
371 TCCTCA 376
346 TCTTCA 351

RESULT 13
AAK20407
ID AAK20407 standard; DNA; 319 BP.
XX
XX AAK20407;
AC
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe SEQ ID NO: 20398.
XX
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Example 4; SEQ ID NO 20398; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention
XX
XX Sequence 319 BP; 69 A; 90 C; 96 G; 64 T; 0 U; 0 Other;
SQ
```


DR WPI; 2003-441521/41.
DR P-P8DB; ADE28455.
XX
PT New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.
XX
PS Claim 24; SEQ ID NO 61; 177pp; English.
XX
CC The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody full length heavy chain cDNA of the invention.
XX
SQ Sequence 364 BP; 73 A; 108 C; 110 G; 73 T; 0 U; 0 Other;
Query Match 62.0%; Score 233; DB 9; Length 364;
Best Local Similarity 82.7%; Pred. No. 1.1e-54;
Matches 305; Conservative 0; Mismatches 55; Indels 9; Gaps 3;
QY 11 CAGCTGCAGCTGCAGAGTGGGCGCCGAGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTC 70
DB |||||
1 CAGGTGCAGCTGCAGAGTGGGCGCCGAGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTC 60
QY 71 ACCTGCGCTGTCTCTGTGGCTCTCTCAGCACTAGTAACTGGTGACCTGGATCGCCAG 130
DB |||||
61 ACCTGCACTGTCTCTGTGGCTC---CATCAGAGTTACTACTGGAGCTGGATCGGGCAG 117
QY 131 CCCCAGGGAAGGACTGGAGTGGATTCGACGATATCTCTGTAGTGGTGGGCCACCAAC 190
DB |||||
118 CCCCAGGGAAGGACTGGAGTGGATTCGATATCTATTACA---GTGGGAGCACCAC 174
QY 191 TACRACCGCTCCCTCAAGAGTGGTCTATTTTCAAGACAGTCCCAAGACCGTTC 250
DB |||||
175 TACAACCCCTCCCTCAAGAGTGGTCTATCCATCATAGACGTCGACGTCGACGAGTTC 234
QY 251 TCCCTGAACCTGAACCTCTGTACCGCCGCGGACACGCGCGTGTATTACTGTGCCAGAGAT 310
DB |||||
235 TCCCTGAAGCTGAGTCTGTGACCGCTCGGACACGCGCGTGTATTACTGTGCCAGAGG 294
QY 311 TGGGCGCAANTAGCTG---GAACACGCTAGCTTCTGGGGCCAGGAGTCTCTGTCACC 367
DB |||||
295 GGGGGCCCTTACGGGTGACTACGGGTGCTCGCCGCCCTGGGGCCAGGAAACCTGTGTCACC 354
QY 368 GTCTCCTCA 376
DB |||||
355 GTCTCCTCA 363

Search completed: June 19, 2004, 06:31:30
Job time : 279 secs

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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 1068194

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Maximum DB seq length: 376

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	237.8	63.2	366	2	US-09-014-880-9
5	237.8	63.2	366	4	US-08-450-363-9
6	217.6	57.9	372	2	US-08-477-553A-46
7	217.2	56.7	363	2	US-08-477-553A-50
8	213.2	56.7	357	2	US-08-652-816A-20
9	209.8	55.8	357	1	US-08-360-125-3
10	209.8	55.8	357	2	US-08-450-578-3
11	209.8	55.8	357	2	US-09-017-628-3
12	209.8	55.8	357	2	US-09-014-880-3
13	209.8	55.8	357	4	US-08-450-363-3
14	209.2	55.6	354	2	US-08-652-816A-23
15	207.8	55.3	369	4	US-08-793-450-3
16	205.4	54.6	321	2	US-08-477-553A-47
17	198.2	52.7	372	2	US-08-477-553A-48
18	198.2	48.0	291	3	US-08-851-362D-13
19	173.2	46.1	297	3	US-09-042-353-151
20	173.2	46.1	297	4	US-08-758-417A-415
21	172.2	45.8	243	3	US-09-042-353-148
22	172.2	45.8	243	4	US-08-758-417A-412
23	171.6	45.6	285	3	US-09-042-353-150
24	171.6	45.6	285	4	US-08-758-417A-414
25	171.4	45.6	282	3	US-09-042-353-149
26	171.4	45.6	282	4	US-08-758-417A-413
27	164.8	43.8	288	3	US-08-851-362D-15

28	160.4	42.7	294	3	US-08-851-362D-3	Sequence 3, Appli
29	159.6	42.4	291	3	US-08-851-362D-11	Sequence 11, Appl
30	159.2	42.3	354	3	US-09-065-059-12	Sequence 12, Appl
31	158.4	42.1	288	3	US-08-851-362D-7	Sequence 7, Appli
32	157.2	41.8	257	3	US-08-767-128-17	Sequence 17, Appl
33	153.2	40.7	291	3	US-08-851-362D-5	Sequence 5, Appli
34	150.4	40.0	300	2	US-08-273-146-68	Sequence 68, Appl
35	150.4	40.0	366	2	US-08-672-345C-87	Sequence 87, Appl
36	150.4	40.0	366	3	US-08-672-345C-89	Sequence 89, Appl
37	150.4	40.0	366	3	US-09-214-095D-101	Sequence 101, App
38	150.4	40.0	366	3	US-09-214-095D-105	Sequence 105, App
39	149	39.6	291	3	US-08-851-362D-9	Sequence 9, Appli
40	148.8	39.6	288	3	US-08-851-362D-17	Sequence 17, Appl
41	147.6	39.3	351	2	US-08-308-494A-14	Sequence 14, Appl
42	145.4	38.7	360	2	US-08-428-197-19	Sequence 19, Appl
43	145.4	38.7	360	5	PCT-US93-10555-19	Sequence 19, Appl
44	143.8	38.2	360	2	US-08-428-197-21	Sequence 21, Appl
45	143.8	38.2	360	2	US-08-428-197-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1

US-08-360-125-9
; Sequence 9, Application US/08360125

; Patent No. 5767246

; GENERAL INFORMATION:

; APPLICANT: Saiko HOSOKAWA

; APPLICANT: Toshiaki TAGAWA

; APPLICANT: Yoko HIRAKAWA

; APPLICANT: No. 5767246/hiko ITO

; APPLICANT: Kazuhiro NAGAIKE

; TITLE OF INVENTION: Human Monoclonal Antibody

; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/360.125

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/905,534

; FILING DATE: June 29, 1992

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8950

; TELEFAX:

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 366 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

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; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-08-360-125-9

Query Match      63.2%; Score 237.8; DB 1; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.6e-65;
Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

QY 11 CAGTCGACGTGCGAGGAGTGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCCGTGCTCC 70
Db 1 CAGTCGACGTGCGAGGAGTGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCCGTGCTCC 60
QY 71 ACCTGCGCTGCTCTGCTGCTGCTGTCAGCAGTAGTA---ACTGCTGGACCTGGATCCGC 127
Db 61 ACCTGCACTGCTCTGCTGCTGCTGCTCAGCAGTAGTAGTACTACTGGGGCTGATCCGC 120
QY 128 CAGCCCCCAGGAGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 187
Db 121 CAGCCCCCAGGAGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 177
QY 188 AACTACAACCCGTCCTCAAGAGTGGAGTGCATCATTTCAAGACACGCTCCAGAACCCAG 247
Db 178 TACTACAACCCGTCCTCAAGAGTGGAGTGCATCATTTCAAGACACGCTCCAGAACCCAG 237
QY 248 TTCTCCCTGAACCTGAACTGTGACCGCGCGGACACGCGCTGTATTACTGTGCGACA 307
Db 238 TTCTCCCTGAAGCTGAGCTGTGACCGCGCGGACACGCGCTGTATTACTGTGCGAGG 297
QY 308 GATTGGGCGCCAAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGAGTCCCTGTGTCAC 367
Db 298 GGGAGCTACGGGGGCTACTACTAGCTATGAGCTGTGGGGCCAGGAGTCCCTGTGTCAC 357
QY 368 GTCTCTCA 376
Db 358 GTCTCTCA 366

RESULT 2
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US-08-450-578-9
; Sequence 9, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845shiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,578
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-9

Query Match 63.2%; Score 237.8; DB 2; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.6e-65;
Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

QY 11 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 70
DB 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
QY 71 ACCTGCGGTGCTCTGTGGTCTGTGACGAGTAGTA---ACTGGTGCAGTGCATCCGC 127
DB 61 ACCTGCACTGTCTGTGGTCTCCATCAGCAGTAGTAGTTACTACTCGGGCTGGATCCGC 120
QY 128 CAGCCCCCAGGAGGAGGAGTGGAGTGGATTGACGTATCTCTGCTAGTGGTGGGCCACC 187
DB 121 CAGCCCCCAGGAGGAGGAGTGGAGTGGATTGGAATATCTATTATA---GTGGAGGACC 177
QY 188 AACTACAAACCGTCCCTCAGAGTGGAGTGCATCATTTTCACAGACAGTCCAGAACAG 247
DB 178 TACTACAAACCGTCCCTCAGAGTGGAGTGCATCACCATATCCGTAGACAGTCCAGAACAG 237
QY 248 TTCTCCCTGAACCTGAACCTGTGACCGCCGACACAGCGCGTATTACTGTGGCCAGA 307
DB 238 TTCTCCCTGAAGCTGAGCTGTGACCGCCGACACAGCGCTGTGATTACTGTGGAGG 297
QY 308 GATTGGGCCCAATAGCTGGAGAACACGCTAGGCTTCTGGGCCCAAGGAGTCCGTGGTACC 367
DB 298 GGGAGCTACGGGGGCTACTACTACGGTATGACGCTCTGGGCCCAAGGAGGACCGGTACC 357
QY 368 GTCTCCTCA 376
DB 358 GTCTCCTCA 366

RESULT 5
US-08-450-363-9
Sequence 9, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
STREET: Wenderoth, Lind & Ponack
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANISLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-9

Query Match 63.2%; Score 237.8; DB 4; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.6e-65;
Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

QY 11 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 70
DB 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60

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Best Local Similarity	86.8%;	Pred. No.	3.8e-59;						
Matches	264;	Conservative	0;	Mismatches	34;	Indels	6;	Gaps	2;

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DB	1	CAGGTGCACCTCAGGAGTCGGGGCCACGAGCTGGTGAAGCCCTTCGGAGACCTCTGTCCTCC	60
QY	71	ACCTGGCTGTCTCTGTGGCTCTGTCTGACAGTAGTAACTGGTGGACCTGTGGATTCGCCAC	130
DB	61	ACCTGCACCTGTCTCTGTGGCTCCGT---CAGTAGTTCCTACTGGAGCTGGATTCGGCAG	117
QY	131	CCCCAGGGAAAGGACTGGAGTGGATTTGGAACGTATCTCTGTGTAGTGTGTGGGGCCACCAAC	190
DB	118	CCCCAGGGAAAGGACCGGAGTGGATTTGGGTATCTATTACA---GTGGGAGCACCAAC	174
QY	191	TACAAACCCGTCCCTCAAGAGTCGAGTCATCTATTTCACAGACACGTCCAAGAACACAGTTC	250
DB	175	TACAAACCCCTCCCTCAGGAGTCGAGTCCACATPATCAGTAGACACGTCCTCAGGAAACCAAGTTC	234
QY	251	TCCTCTGAACCTGAACTCTGTGACCGCCGGGACACGGCCGTGTATTACTGTGCCAGAGAT	310
DB	235	TCCTCTGAAGCTGGGCTCTGTGACCGCTGGGACACGGCCGTGTATTACTGTGGAGATT	294
QY	311	TTGGG	314
DB	295	TTGGG	298

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MOLECULE TYPE: DNA (genomic)
US-08-477-553A-50

Query Match 57.7%; Score 217; DB 2; Length 363;
Best Local Similarity 79.9%; Pred. No. 5.8e-59;
Matches 295; Conservative 0; Mismatches 65; Indels 9; Gaps 3;

PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-816A-20

Query Match 56.7%; Score 213.2; DB 2; Length 357;
Best Local Similarity 80.1%; Pred. No. 9.1e-56;
Matches 290; Conservative 0; Mismatches 63; Indels 9; Gaps 3;

QY 11 CAGCTGCAGCTGCAGAGTCCGGCCAGAGTGGTGAAGCTTCGGAGACCCCTGTCCCTC 70
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QY 71 ACCTGGCTGTCTCTGGTGGCTCTGTGACAGTAGTAACTCTCTGGTAGTGTGGGGCCAGCAG 130
DB 61 ACCTGGCACTGTCTCTGGTGAATC---CATCAGTAGTGTCTGGAGCTGGATCCGGCAG 117
QY 131 CCCCAGGAGGAGGACTCGAGTGGATTCGACGATCTCTCTGGTAGTGTGGGGCCAGCAGC 190
DB 118 CCCCAGGAGGAGGACTCGAGTGGATTCGACGATCTCTCTGGTAGTGTGGGGCCAGCAGC 174
QY 191 TACACCCGCTCCCTCAAGAGTGCAGTCACTTTCACAGACAGCTGCAGACACAGTTC 250
DB 175 TCCACCCCTCCCTCAAGAGTGCAGTCACTTTCACAGACAGCTGCAGACACAGTTC 234
QY 251 TCCCTGAACCTGAACTCTGTGACCCGCGGACACGCGCTGTATTACTGTGCCAGAGAT 310
DB 235 TCCCTGAAGCTGAGCTCTGTGACCCGCGGACACGCGCTGTATTACTGTGGGGGTGC 294
QY 311 TGGGCCCAATAGCTGGAACAAAGCTAGGCTTCGGGGCCAGGAGTTCCTGTGTCACCGTC 370
DB 295 GGTGCCTA---CGATAATTACGGTATAGACCTCTCGGGCAAGGACCCCTGTGTCACCGTC 351
QY 371 TC 372
DB 352 TC 353

RESULT 9
US-08-360-125-3
Sequence 3, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246biko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42

QY 11 CAGCTGCAGCTGCAGAGTCCGGCCAGAGTGGTGAAGCTTCGGAGACCCCTGTCCCTC 70
DB 1 CAGGTGCAGCTGCAGAGTCCAGGCTCAGGCTTGGTGAAGCTTCGGAGACCCCTGTCCCTC 60
QY 71 ACCTGGCTGTCTCTGGTGGCTCTGTGACAGTAGTAACTCTCTGGTAGTGTGGGGCCAG 130
DB 61 ACCTGGCACTGTCTCTGGTGAATC---CATCAGTAGTGTCTGGAGCTGGATCCGGCAG 117
QY 131 CCCCAGGAGGAGGACTCGAGTGGATTCGACGATCTCTCTGGTAGTGTGGGGCCAGCAGC 190
DB 118 CCCCAGGAGGAGGACTCGAGTGGATTCGACGATCTCTCTGGTAGTGTGGGGCCAGCAGC 174
QY 191 TACACCCGCTCCCTCAAGAGTGCAGTCACTTTCACAGACAGCTGCAGACACAGTTC 250
DB 175 TCCACCCCTCCCTCAAGAGTGCAGTCACTTTCACAGACAGCTGCAGACACAGTTC 234
QY 251 TCCCTGAACCTGAACTCTGTGACCCGCGGACACGCGCTGTATTACTGTGCCAGAGAT 310
DB 235 TCCCTGAAGCTGAGCTCTGTGACCCGCGGACACGCGCTGTATTACTGTGGGGGTGC 294
QY 311 TGGGCCCAATAGCTGGAACAAAGCTAGGCTTCGGGGCCAGGAGTTCCTGTGTCACCGTC 370
DB 295 GGTGCCTA---CGATAATTACGGTATAGACCTCTCGGGCAAGGACCCCTGTGTCACCGTC 354
QY 368 GTCTCCTCA 376
DB 355 GTCTCCTCA 363

RESULT 8
US-08-652-816A-20
Sequence 20, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and methods.
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (SFO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL LINE: antibody GAE
; ORGANELLE:
; IMMEDIATE SOURCE:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:

; RELEVANT RESIDUES IN SEQ ID NO:
; US-08-360-125-3
; Query Match 55.8%; Score 209.8; DB 1; Length 357;
; Best Local Similarity 79.1%; Pred. No. 1.1e-56;
; Matches 292; Conservative 0; Mismatches 62; Indels 15; Gaps 3;
; QY 11 CAGCTGCAGCTGCAGGAGTGGGCCCCAGGAGTGGTGAAGCCTTCGGCAGACCCCTGTCCCTC 70
; DB 1 CAGGTGCAGCTGCAGGAGTGGGCCCCAGGAGTGGTGAAGCCTTCACAGACCCCTGTCCCTC 60
; QY 71 ACCTGGCGCTCTCTCTGGTGGCTCTGTTCAGCA---GTAGTAACTGGTGGGAGTGGATCCG 127
; DB 61 ACCTGGCACTGTCTCTGGTGGCTCTCATCAGCAGTGTGGTGTCTTCTACTGGAACTGGATCCG 120
; QY 128 CAGCCCCCAGGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 187
; DB 121 CAGCACCACGAGGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGG 177
; QY 188 AACTACAAACCCCTCCCTCAAGAGTGCAGTCAATTCACAAACAGACAGTCCACAGAACAG 247
; DB 178 TACTACAAACCCCTCCCTCAAGAGTGCAGTCAATTCACAAACAGACAGTCCACAGAACAG 237
; QY 248 TTCTCCCTGAACCTGAACCTGTGACCGCCGCGGAGCAGCGCGTGTATTACTGTGCCAGA 307
; DB 238 TTCTCCCTGAAGCTGAGCTCTCTGACTGCGCGGAGCAGCGCGTGTATTACTGTGCCAGA 297
; QY 308 GATTGGGCCCCAATAGCTGGAAACAGCTAGGCTTCTGGGGCCAGGAGTCCCTGGTCAAC 367
; DB 298 TCTACCCGACTACGGG-----GGGCTGACTACTGGGGCCAGGAGCAACAATGGTCAAC 348
; QY 368 GTCTCCTCA 376
; DB 349 GTCTCTTCA 357
; RESULT 10
; US-08-450-578-3
; Sequence 3, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845biko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,578
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-3

Query Match 55.8%; Score 209.8; DB 2; Length 357;
Best Local Similarity 79.1%; Pred. No. 1.1e-56;
Matches 292; Conservative 0; Mismatches 62; Indels 15; Gaps 3;

QY 11 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTGGGAGACCCCTGTCCCTC 70
DB 1 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTGCACAGACCCCTGTCCCTC 60
QY 71 ACCTGGCTGTCTCTGGTGGCTCTGTCTGCA---GTAGTAAGTGGTGGACCTGGATCCGC 127
DB 61 ACCTGCACCTGTCTCTGGTGGCTCTGTCTGCA---GTAGTAAGTGGTGGACCTGGATCCGC 120
QY 128 CAGCCCCCAGGAGGAGTGGAGTGGATTTGGAAGTATCTCTGTGTAGTGGTGGGCCACC 187
DB 121 CAGCAGCCAGGAGGAGGCTGGAGTGGATTTGGTATCTATTACA---GTGGGAGCACC 177
QY 188 AACTACACCCGTCCTCAGAGTGCAGTCATCTTTCACAGACACCTCCAGAACCCAG 247
DB 178 TACTACACCCGTCCTCAGAGTGCAGTCATCTTTCACAGACACCTCCAGAACCCAG 237
QY 248 TTCTCCCTGAACCTGAACCTCTGTGACCGCCCGGACACGGCCGTGTATTACTGTGCCAGA 307
DB 238 TTCTCCCTGAACCTGCAGCTCTGTGACCTCCGCGGACACGGCCGTGTATTACTGTGCCAG 297
QY 308 GATTGGGCCCAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCTACC 367
DB 298 TCTACCCGACTACGGG-----GGGCTGACTACTGGGGCCAGGGAACAATGTCTACC 348
QY 368 GTCTCTCTCA 376
DB 349 GTCTCTCTCA 357

QY 248 TTCTCCCTGAACCTGAACCTCTGTGACCGCCCGGACACGGCCGTGTATTACTGTGCCAGA 307
DB 238 TTCTCCCTGAACCTGCAGCTCTGTGACTGCCGGGACACGGCCGTGTATTACTGTGCCAGG 297
QY 308 GATTGGGCCCAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCTACC 367
DB 298 TCTACCCGACTACGGG-----GGGCTGACTACTGGGGCCAGGGAACAATGTCTACC 348
QY 368 GTCTCTCTCA 376
DB 349 GTCTCTCTCA 357

RESULT 11
US-09-017-628-3
; Sequence 3, Application US/09017628
; Patent No. 5930287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287ihiko
; APPLICANT: NAGAIKE, Kazuhiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; CELL TYPE: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-3

Query Match 55.8%; Score 209.8; DB 2; Length 357;
Best Local Similarity 79.1%; Pred. No. 1.1e-56;
Matches 292; Conservative 0; Mismatches 62; Indels 15; Gaps 3;

QY 11 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTGGGAGACCCCTGTCCCTC 70
DB 1 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTGCACAGACCCCTGTCCCTC 60
QY 71 ACCTGGCTGTCTCTGGTGGCTCTGTCTGCA---GTAGTAAGTGGTGGACCTGGATCCGC 127
DB 61 ACCTGCACCTGTCTCTGGTGGCTCTGTCTGCA---GTAGTAAGTGGTGGACCTGGATCCGC 120
QY 128 CAGCCCCCAGGAGGAGTGGAGTGGATTTGGAAGTATCTCTGTGTAGTGGTGGGCCACC 187
DB 121 CAGCAGCCAGGAGGAGGCTGGAGTGGATTTGGTATCTATTACA---GTGGGAGCACC 177
QY 188 AACTACACCCGTCCTCAGAGTGCAGTCATCTTTCACAGACACCTCCAGAACCCAG 247
DB 178 TACTACACCCGTCCTCAGAGTGCAGTCATCTTTCACAGACACCTCCAGAACCCAG 237
QY 248 TTCTCCCTGAACCTGAACCTCTGTGACCGCCCGGACACGGCCGTGTATTACTGTGCCAGA 307
DB 238 TTCTCCCTGAACCTGCAGCTCTGTGACCTCCGCGGACACGGCCGTGTATTACTGTGCCAG 297
QY 308 GATTGGGCCCAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCTACC 367
DB 298 TCTACCCGACTACGGG-----GGGCTGACTACTGGGGCCAGGGAACAATGTCTACC 348
QY 368 GTCTCTCTCA 376
DB 349 GTCTCTCTCA 357

RESULT 12
US-09-014-880-3
; Sequence 3, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; US-09-014-880-3
Query Match 55.8%; Score 209.8; DB 2; Length 357;
Best Local Similarity 79.1%; Pred. No. 1.le-56;
Matches 292; Conservative 0; Mismatches 62; Indels 15; Gaps 3;
QY 11 CAGCTGCAGTCGAGGTCGGGCGCCAGGAGTGGTCAAGCCTTCGGAGACCCCTGTCCCTC 70
Db |||||
1 CAGGTGCAGTCGAGGTCGGGCGCCAGGAGTGGTCAAGCCTTCAGACCCCTGTCCCTC 60
QY 71 ACCTGGCTGTCTCTGGTGGCTCTGTACGCA---GTAGTACTGTGGACCTGGATCCGC 127
Db |||||
61 ACCCTGCAGTGTCTCTGGTGGCTTCCATCAGCAGTGTGGTTTCTACTGGAAGTGGATCCGC 120
QY 128 CAGCCCGCCAGGAGGAGTGGAGTGGATTTGACCTATCTCTGTAGTGGTGGGCGCAC 187
Db |||||
121 CAGCAGCCAGGAGGAGTGGAGTGGATTTGGTACATCTATTACA---GTGGGAGCAC 177
QY 188 AACTACAAACCCCTCCCTCAAGAGTGCAGTCATCTTCAAGACACGTCACAAAGCCAG 247
Db |||||

Db 178 TACTACAAACCCCTCCCTCAAGAGTGCAGTTCACCATATCGCTAGACACGCTTAAGAGCCAG 237
QY 248 TTCTCCCTGAACCTGAACCTCTGTGACCGCGCGGACACCGGCGCTGTATTACTGTGCCAGA 307
Db |||||
238 TTCTCCCTGAAGCTGAGCTCTCTGACTGCGCGGACACCGGCGCTGTATTACTGTGCCAGG 297
QY 308 GATTGGGGCCCAATAGCTGGAACCAACCTAGGCTTCTGGGGCCAGGAGTCCCTGTGTCAAC 367
Db |||||
298 TCTACCCGACTACGGG-----GGGCTGACTACTTGGGGCCAGGAGCAATGGTCACC 348
QY 368 GTCTCTCTCA 376
Db |||||
349 GTCTCTTCA 357

RESULT 13
US-08-450-363-3
; Sequence 3, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434/hiiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:


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Db 178 TACAAACCGCTCCTCAGAGTGGAGTCCACCATATCAGGAGCGCATCCAAAGAACGAGTTT 237
Qy 251 TCCCTGAACCTGAACCTCTGTGACCGCCGCGGACACGCGCGTGTATTACTGTGCGCAGAGAT 310
Db 238 TTCTGTGAGCTGACTCTGTGACCGCCGCGGACACGCGCGTGTATTACTGTGCGGAGTCT 297
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Db 298 GAG-----CCTACCGCCCAACTTTGATTCTTGGGCGCAGGGGCAACCGCTGTCAACCGTC 348
Qy 371 TC 372
Db 349 TC 350

RESULT 15
US-08-793-450-3
; Sequence 3, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; CITY: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN P.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..369
; OTHER INFORMATION: /product= "IMMUNOGLOBIN VARIABLE
; OTHER INFORMATION: REGION"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 91..105
; OTHER INFORMATION: /label= CDR1
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: 148..195
; OTHER INFORMATION: /label= CDR2
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 292..336
; OTHER INFORMATION: /standard_name= "CDR3"
US-08-793-450-3

Query Match 55.3%; Score 207.8; DB 4; Length 369;
Best Local Similarity 78.1%; Pred. No. 4.6e-56;
Matches 293; Conservative 0; Mismatches 67; Indels 15; Gaps 3;

Qy 11 CAGCTGCAGCTGCAGGAGTCGGGCCCAAGGAGTGTGAAGCTTCGGAGACCCCTGTCTCCCTC 70
Db 1 CAGGTCCAACTGCAGCAGTGGGGCGCAGGACTGTTGAAGCTTCGGAGACCCCTGTCTCCCTC 60
Qy 71 ACTTGCCTGTCTCTGTGTGCTCTGTTCAGCAGTAGTAGTAACCTGGTGGACCTGGATCCGCGAG 130
Db 61 ACTTGCACTGTCTATGGTGGCTC---CTTCAGTGGTTACTACTCTGAGCTGGATCCGCGAG 117
Qy 131 CCCCCAGGGAAGGACTCGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCCAACCAAC 190
Db 118 CCCCCAGGGAAGGGGCTGGAGTGGATTGGGGAATCAATCATAGTGAAG---CACCAAC 174
Qy 191 TACAACCCCGTCCCTCAAGAGTTCGAGTGCATCATTTTCAAGACACAGCTCCAAAGAACCAATTC 250
Db 175 TACAACCCCGTCCCTCAAGAGTTCGAGTGCATCATTTTCAAGACACAGCTCCAAAGAACCAATTC 234
Qy 251 TCCCTGAACCTGAACCTCTGTGACCGCCGCGGACACGCGCGTGTATTACTGTGCGCAGAGAT 310
Db 235 TCCCTGAACCTGAACCTCTGTGACCGCCGCGGACACGCGCGTGTATTACTGTGCGGAGGCC 294
Qy 311 TGGGCCCAATA-----GCTGGAACCAACGCTAGGCTTCTGGGGCCCAAGGAGTCTCTG 361
Db 295 CCAGATGATTAATGGAAGTATCATGGGACTGTGGTTCGACCCCTGGGGCCCAAGGTACCACT 354
Qy 362 GTCACCGTCTCCCTCA 376
Db 355 GTCACCGTCTCCCTCA 369

Search completed: June 19, 2004, 07:32:31
Job time : 64 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 07:02:32 ; Search time 283 Seconds
(without alignments)
6086.536 Million cell updates/sec

Title: US-09-019-441A-3_COPY_48_423

Perfect score: 376
Sequence: 1 ggcctgtccagctgcagc.....tctgtgacacctctctctca 376

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 2667516

Minimum DB seq length: 0
Maximum DB seq length: 376

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	249.2	56.3	361	16	US-10-309-762-208
2	246	55.4	361	16	US-10-309-762-118
3	246	55.4	361	16	US-10-309-762-182
4	246	55.4	361	16	US-10-309-762-206
5	241.4	64.2	356	17	US-10-038-591-33
6	235.4	62.6	356	17	US-10-038-591-57
7	235.2	62.6	356	17	US-10-388-214A-35
8	235.2	62.6	356	17	US-10-388-214A-37
9	235.2	62.6	362	9	US-09-864-761-32297
10	234.8	62.4	367	16	US-10-309-762-183
11	234.8	62.4	367	16	US-10-309-762-196
12	234.6	62.4	364	13	US-10-302-088-97
13	233.8	62.2	319	9	US-09-864-761-28401
14	233.2	62.0	367	16	US-10-309-762-116

15	233.2	62.0	367	16	US-10-309-762-181
16	233	62.0	352	16	US-10-309-762-203
17	233	62.0	364	13	US-10-292-088-65
18	233	62.0	364	13	US-10-292-088-81
19	231.8	61.6	361	16	US-10-309-762-193
20	231.6	61.6	357	13	US-10-292-088-17
21	231.2	61.5	370	16	US-10-309-762-186
22	229.8	61.1	367	16	US-10-309-762-195
23	228.2	60.7	363	13	US-10-292-088-25
24	228.2	60.7	363	15	US-10-067-800-59
25	228	60.6	370	16	US-10-309-762-185
26	226.4	60.2	349	12	US-10-269-711-2
27	225.8	60.1	375	13	US-10-371-942-117
28	225.4	59.9	293	17	US-10-038-591-43
29	225.4	59.9	364	17	US-10-038-591-59
30	223.8	59.5	293	17	US-10-038-591-35
31	223.2	59.4	369	13	US-10-371-942-101
32	223.2	59.4	373	16	US-10-309-762-192
33	222.6	59.2	358	15	US-10-330-613-27
34	222.6	59.2	358	15	US-10-330-530-27
35	222.2	59.1	370	16	US-10-309-762-204
36	221.8	59.0	361	16	US-10-309-762-191
37	221.8	59.0	364	15	US-10-330-613-11
38	221.8	59.0	364	15	US-10-330-613-39
39	221.8	59.0	364	15	US-10-330-530-11
40	220.8	58.7	324	9	US-09-864-761-31244
41	220.4	58.6	367	16	US-10-309-762-198
42	220.4	58.6	367	16	US-10-309-762-210
43	220.2	58.6	352	15	US-10-330-613-15
44	220.2	58.6	352	15	US-10-330-530-15
45	220.2	58.6	352	15	US-10-330-530-15

ALIGNMENTS

RESULT 1
US-10-309-762-208
; Sequence 208, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-208

Query Match	66.3%;	Score	249.2;	DB	16;	Length	361;
Best Local Similarity	83.9%;	Pred. No.	6.6e-68;				
Mismatches	307;	Conservative	0;	Mismatches	53;	Indels	6;
Gaps	2;						
QY	11	CAGTCCAGCTGCTCTCTGTGGTGGTCTGTGACAGTAGTAATCTGGAGTGGATCCGCCAG	70				
Db	1	CAGTCCAGCTGCTCTCTGTGGTGGTCTGTGACAGTAGTAATCTGGAGTGGATCCGCCAG	60				
QY	71	ACCTGCGCTGTCTCTGTGGTGGTCTGTGACAGTAGTAATCTGGAGTGGATCCGCCAG	130				
Db	61	ACCTGCGCTGTCTCTGTGGTGGTCTGTGACAGTAGTAATCTGGAGTGGATCCGCCAG	117				
QY	131	CCCCCAGGGAAGGAGCTGGAGTGGATCTCTGTGGTGGTGGATCTCTGTGGTGGGCGCCACCAAC	190				

Db 118 CCGCGCGGAGGAGTGGAGTGGATGGCGGTATCT---ATACCAGTGGGAGCACCAC 174
Qy 191 TACAACCCGTCCTCAAGAGTCAGTGCATCATTTCAAGACACAGCTCAAGAACAGTTC 250
Db 175 TACAACCCCTCCCTCAAGAGTCAGTGCATCATTTCAAGACACAGCTCAAGAACAGTTC 234
Qy 251 TCCTGAACTGAACTCTGTGACCGCGGACACAGCGCGGTATTAATCTGTGCGAGAT 310
Db 235 TCCTGAACTGAACTCTGTGACCGCGGACACAGCGCGGTATTAATCTGTGCGAGAT 294
Qy 311 TGGGCCCCAATAGCTGGAACACAGCTAGGCTTCTGGGCGCAGGAGTCTGTGTCACGTC 370
Db 295 CAGGATTTTGGAGTGGTACCTCTGGAGCTCTGGGCGCAGGAGTCTGTGTCACGTC 354
Qy 371 TCCTCA 376
Db 355 TCCTCA 360

RESULT 2
US-10-309-762-118
; Sequence 118, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-118

Query Match 65.4%; Score 246; DB 16; Length 361;
Best Local Similarity 83.3%; Pred. No. 6.6e-67;
Matches 305; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

Qy 11 CAGCTGCAGCTGCAGGAGTGGGCGGCGGAGTGGTGAAGCTTCGGAGACCTGTGCTC 70
Db 1 CAGGTGCAGCTGCAGGAGTGGGCGGCGGAGTGGTGAAGCTTCGGAGACCTGTGCTC 60
Qy 71 ACCTGCGCTGTCTGTGGTGGCTCTGTGACAGTGTAACTGTGAGTGGTGGTGGTGGT 130
Db 61 ACCTGCACTGTCTGTGGTGGCTC---CATCAGTGTACTGTGAGTGGTGGTGGTGGT 117
Qy 131 CCGCGGAGGAGGAGTGGAGTGGATGGAGCTGTCTGTGAGTGGTGGTGGTGGTGGT 190
Db 118 CCGCGGAGGAGGAGTGGAGTGGATGGAGCTGTCTGTGAGTGGTGGTGGTGGTGGT 174
Qy 191 TACAACCCGTCCTCAAGAGTGGAGTGCATCATTTCAAGACACAGCTCAAGAACAGTTC 250
Db 175 TACAACCCCTCCCTCAAGAGTGGAGTGCATCATTTCAAGACACAGCTCAAGAACAGTTC 234
Qy 251 TCCTGAACTGAACTCTGTGACCGCGGACACAGCGCGGTATTAATCTGTGCGAGAT 310
Db 235 TCCTGAACTGAACTCTGTGACCGCGGACACAGCGCGGTATTAATCTGTGCGAGAT 294
Qy 311 TGGGCCCCAATAGCTGGAACACAGCTAGGCTTCTGGGCGCAGGAGTCTGTGTCACGTC 370
Db 295 CAGGATTTTGGAGTGGTACCTCTGGAGCTCTGGGCGCAGGAGTCTGTGTCACGTC 354
Qy 371 TCCTCA 376
Db 355 TCCTCA 360

Db 355 TCCTCA 360
RESULT 3
US-10-309-762-182
; Sequence 182, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-182

Query Match 65.4%; Score 246; DB 16; Length 361;
Best Local Similarity 83.3%; Pred. No. 6.6e-67;
Matches 305; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

Qy 11 CAGCTGCAGCTGCAGGAGTGGGCGGCGGAGTGGTGAAGCTTCGGAGACCTGTGCTC 70
Db 1 CAGGTGCAGCTGCAGGAGTGGGCGGCGGAGTGGTGAAGCTTCGGAGACCTGTGCTC 60
Qy 71 ACCTGCGCTGTCTGTGGTGGCTCTGTGACAGTGTAACTGTGAGTGGTGGTGGTGGT 130
Db 61 ACCTGCACTGTCTGTGGTGGCTC---CATCAGTGTACTGTGAGTGGTGGTGGTGGT 117
Qy 131 CCGCGGAGGAGGAGTGGAGTGGATGGAGCTGTCTGTGAGTGGTGGTGGTGGTGGT 190
Db 118 CCGCGGAGGAGGAGTGGAGTGGATGGAGCTGTCTGTGAGTGGTGGTGGTGGTGGT 174
Qy 191 TACAACCCGTCCTCAAGAGTGGAGTGCATCATTTCAAGACACAGCTCAAGAACAGTTC 250
Db 175 TACAACCCCTCCCTCAAGAGTGGAGTGCATCATTTCAAGACACAGCTCAAGAACAGTTC 234
Qy 251 TCCTGAACTGAACTCTGTGACCGCGGACACAGCGCGGTATTAATCTGTGCGAGAT 310
Db 235 TCCTGAACTGAACTCTGTGACCGCGGACACAGCGCGGTATTAATCTGTGCGAGAT 294
Qy 311 TGGGCCCCAATAGCTGGAACACAGCTAGGCTTCTGGGCGCAGGAGTCTGTGTCACGTC 370
Db 295 CAGGATTTTGGAGTGGTACCTCTGGAGCTCTGGGCGCAGGAGTCTGTGTCACGTC 354
Qy 371 TCCTCA 376
Db 355 TCCTCA 360

RESULT 4
US-10-309-762-206
; Sequence 206, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A


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; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-206

Query Match          65.4%; Score 246; DB 16; Length 361;
Best Local Similarity 83.3%; Pred. No. 6e-67;
Matches 305; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 11 CAGCTGCGAGCTGCAGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 70
DB 1 CAGGTGCAGCTGCAGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60

QY 71 ACCTGGCTGTCTCTCTGGTGGCTCTGTGAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 130
DB 61 ACCTGGCTGTCTCTCTGGTGGCTCTGTGAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 120

QY 131 CCCCAGGGAAGGACTGGAGTGGATTTGGAGGATCTCTCTGTAGTGGTGGGCCACCAAC 190
DB 121 CCCCAGGGAAGGACTGGAGTGGATTTGGAGGATCTCTCTGTAGTGGTGGGCCACCAAC 177

QY 191 TACAACCCGTCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGTCCTCAAGAACCACTTC 250
DB 178 TACAACCCGTCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGTCCTCAAGAACCACTTC 237

QY 251 TCCCTGAACCTGAACCTCTGTGACCGCCGAGACACGCGCTGTATTACTGTGCCAGAGA 309
DB 238 TCCCTGAACCTGAACCTCTGTGACCGCCGAGACACGCGCTGTATTACTGTGCCAGAGA 296

RESULT 6
US-10-038-591-57
; Sequence 57, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: sequence
; NAME/KEY: modified_base
; LOCATION: (337)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-038-591-57

Query Match          62.6%; Score 235.4; DB 17; Length 358;
Best Local Similarity 82.5%; Pred. No. 1.4e-63;
Matches 302; Conservative 4; Mismatches 51; Indels 9; Gaps 3;

QY 11 CAGCTGAGCTGCAGAGTTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 70
DB 1 CAGGTGCAGCTGCAGAGTTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60

QY 71 ACCTGGCTGTCTCTCTGGTGGCTCTGTGAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 130
DB 61 ACCTGGCTGTCTCTCTGGTGGCTCTGTGAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 117

QY 131 CCCCAGGGAAGGACTGGAGTGGATTTGGAGGATCTCTCTGTAGTGGTGGGCCACCAAC 190
DB 118 CCCCAGGGAAGGACTGGAGTGGATTTGGAGGATCTCTCTGTAGTGGTGGGCCACCAAC 174

QY 191 TACAACCCGTCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGTCCTCAAGAACCACTTC 250
DB 175 TACAACCCGTCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGTCCTCAAGAACCACTTC 234

; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-206

Query Match          64.2%; Score 241.4; DB 17; Length 296;
Best Local Similarity 90.3%; Pred. No. 1.7e-65;
Matches 270; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 11 CAGCTGCGAGCTGCAGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 70
DB 1 CAGGTGCAGCTGCAGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60

QY 71 ACCTGGCTGTCTCTCTGGTGGCTCTGTGAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 130
DB 61 ACCTGGCTGTCTCTCTGGTGGCTCTGTGAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 117

QY 131 CCCCAGGGAAGGACTGGAGTGGATTTGGAGGATCTCTCTGTAGTGGTGGGCCACCAAC 190
DB 121 CCCCAGGGAAGGACTGGAGTGGATTTGGAGGATCTCTCTGTAGTGGTGGGCCACCAAC 177

QY 191 TACAACCCGTCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGTCCTCAAGAACCACTTC 250
DB 178 TACAACCCGTCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGTCCTCAAGAACCACTTC 237

QY 251 TCCCTGAACCTGAACCTCTGTGACCGCCGAGACACGCGCTGTATTACTGTGCCAGAGA 310
DB 235 TCCCTGAACCTGAACCTCTGTGACCGCCGAGACACGCGCTGTATTACTGTGCCAGAGA 294

QY 311 TGGGCCCAATAGCTGGGAACAGCTAGGCTTCTGGGCCAGGAGTCTGTGTACCCCTC 370
DB 295 GGGCAGTGGCTGGAAGACTACGCTATGAGCGTCTGGGCCAGGAGACCAACCGTCAACCCCTC 354

QY 371 TCCCTCA 376
DB 355 TCCCTCA 360

RESULT 5
US-10-038-591-33
; Sequence 33, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-591-33
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QY 251 TCCCTGACCTGAACCTCTGTGACCGCGCGGACACGGCGGTGTATTACTGTGCGACAGAT 310
Db 235 TCCCTGAAGCTGACCTCTGTGACCGCGCGGACACGGCGGTGTATTACTGTGCGCGTA 291
QY 311 TGGGCGCCAAATAGCTGGGAACACGCTAGGCTTCTGGGCGCAGGGAGTCTCTGTACCGCTC 370
Db 292 ACGATTTTGGAGTGGTTATTATCTTTGACTACTGGGCGCCAGGACGCTCTGTACCGCTC 351
QY 371 TCCTCA 376
Db 352 TCCTCA 357

RESULT 7

US-10-388-214A-35

; Sequence 35, Application US/10388214A

; Publication No. US20040082762A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Gurig

; APPLICANT: Saldanha, Jose

; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA

; FILE REFERENCE: ELM-004

; CURRENT APPLICATION NUMBER: US/10/388,214A

; CURRENT FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US 60/363,751

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 35

; LENGTH: 356

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(356)

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: (1)...(57)

; US-10-388-214A-35

Query Match 62.6%; Score 235.2; DB 17; Length 356;
Best Local Similarity 89.1%; Pred. No. 1.6e-63;
Matches 278; Conservative 0; Mismatches 28; Indels 6; Gaps 2;

QY 1 GGTCTGTCCAGCTGACAGTGCAGGAGTGGGCGCCAGAGTGTGAGCGCTTCGGAGAC 60
Db 48 GGTCTGTCCAGCTGACAGTGCAGGAGTGGGCGCCAGAGTGTGAGCGCTTCGGAGAC 107
QY 61 CCTGTCCCTCACTGCGCTGTCTGTGGTGGCTCTGTGACGA--GTAGTAACTGGTGAC 117
Db 108 CCTGTCCCTCACTGCGCTGTCTGTGGTGGCTCTGTGACGA--GTAGTAACTGGTGAC 167

QY 118 CTGGATCCGCGCAGCCCGCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGG 177
Db 168 CTGGATCCGCGCAGCCCGCCAGGGAAGGGACTGGAGTGGATTGGATATCTATTACA--G 224
QY 178 TGGGCGCCACCACTACACCGCTCCCTCAAGAGTCGAGTCATGATTTTCACAGACACGTC 237
Db 225 TGGGAGCACCACCACTACACCGCTCCCTCAAGAGTCGAGTCATGATTTTCACAGACACGTC 284
QY 238 CAAGAACCAGTTCCTCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGGCGGTGTATTA 297
Db 285 CAAGAACCAGTTCCTCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGGCGGTGTATTA 344

QY 298 CTGTGCCAGAGA 309

Db 345 CTGTGCCAGAGA 356

RESULT 8

US-10-388-214A-37

; Sequence 37, Application US/10388214A

; Publication No. US20040082762A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
; FILE REFERENCE: ELM-004
; CURRENT APPLICATION NUMBER: US/10/388,214A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/363,751
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 356
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(356)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(57)
; US-10-388-214A-37

Query Match 62.6%; Score 235.2; DB 17; Length 356;
Best Local Similarity 89.1%; Pred. No. 1.6e-63;
Matches 278; Conservative 0; Mismatches 28; Indels 6; Gaps 2;

QY 1 GGTCTGTCCAGCTGACAGTGCAGGAGTGGGCGCCAGAGTGTGAGCGCTTCGGAGAC 60
Db 48 GGTCTGTCCAGCTGACAGTGCAGGAGTGGGCGCCAGAGTGTGAGCGCTTCGGAGAC 107
QY 61 CCTGTCCCTCACTGCGCTGTCTGTGGTGGCTCTGTGACGA--GTAGTAACTGGTGAC 117
Db 108 CCTGTCCCTCACTGCGCTGTCTGTGGTGGCTCTGTGACGA--GTAGTAACTGGTGAC 167
QY 118 CTGGATCCGCGCAGCCCGCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGG 177
Db 168 CTGGATCCGCGCAGCCCGCCAGGGAAGGGACTGGAGTGGATTGGATATCTATTATA--G 224
QY 178 TGGGCGCCACCACTACACCGCTCCCTCAAGAGTCGAGTCATCATTTTCACAGACACGTC 237
Db 225 TGGGAGCACCACCACTACACCGCTCCCTCAAGAGTCGAGTCATCATTTTCACAGACACGTC 284
QY 238 CAAGAACCAGTTCCTCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGGCGGTGTATTA 297
Db 285 CAAGAACCAGTTCCTCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGGCGGTGTATTA 344
QY 298 CTGTGCCAGAGA 309
Db 345 CTGTGCCAGAGA 356

RESULT 9

US-09-864-761-32297

; Sequence 32297, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366


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; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 167
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-196

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Query Match	62.4%	Score	234.8	DB	16	Length	367
Best Local Similarity	82.8%	Pred. No.	2.1e-63				
Matches	308	Conservative	0	Mismatches	52	Indels	12
						Gaps	3

QY	11	CAGCTGCAGCTGCAGGAGTCCGGGCCACGAGTGGTGAAGCTTCGGAGACCCCTGTCCTC	70
DB	1		
		CAGGTGCAGCTGCAGGAGTCCGGGCCACGAGTGGTGAAGCTTCGGAGACCCCTGTCCTC	60
QY	71	ACCTGGCTCTCTCTGGTGGCTCTGTCCAGCAGTAGTAACTGGTGGGACTCGATCCGCAG	130
DB	61		
		ACCTGCACCTCTCTGGTGGCTC---CATCAGTAGTTACTACTGGAGCTGSAATCCGGCAG	117
QY	131	CCCCCAGGGAAGGACCTGGAGTGATTTGGACGATCTCTGGTAGTGGTGGGCCACCAAC	190
DB	118		
		CCCCCAGGGAAGGACCTGGAGTGATTTGGGTATATCTATTACA---GTGGAGACCCAC	174
QY	191	TACAACCCGTCCTCAAGAGTCCAGTCAATCATTTCAAGACAGCTCCAAGAACCACTTC	250
DB	175		
		TACAACCCCTCCCTCAAGAGTCCAGTCAACATATCAGTAGACAGCTCCAAGAACCACTTC	234
QY	251	TCCTGAACCTGAACCTGTGACCGCCGGACACCGCCCTGTATTACTGTGCCAGAGAT	310
DB	235		
		TCCTTGAAGCTGAGCTCTGTGACCGCTGCGGACACCGCCCTGTATTACTGTGGAGAAGG	294
QY	311	TGGGGCCCAAT-----AGCTGGAAACAACGCTAGGCTTCTGGGCCCAGGAGATCCTGCTC	364
DB	295		
		GGGTAGATATTTTGACTGGTTATGACTATTTGACTACTGGGGCCAGGAGAACCTGTGTC	354
QY	365	ACCGTCTCCTCA	376
DB	355	ACCGTCTCCTCA	366

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RESULT 12
US-10-292-088-97
; Sequence 97, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 97
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-292-088-97

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Query Match	62.4%	Score 234.6	DB 13	Length 364
Best Local Similarity	82.9%	Pred. No. 2.4e+63		
Matches 306	Conservative	0	Mismatches 54	Indels 9
Gaps 3				

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Db	1		60
QY	71	ACCTGGCCTCTCTCTGGTGGCTCTGTTCAGCAGTAGTAATCGTGGACCTGGATCGGCAG	130
Db	61	ACCTGCACCTGTCTCTGGTGGCTC---CATCAGTAGTACTACTGGAGCTGGATCGGCAG	117
QY	131	CCCCCAGGGAAGGACCTGGAGTGGATTGCACTATCTCTGGTAGTGGTGGGCCACCAAC	190
Db	118	CCCCCAGGGAAGGACCTGGAGTGGATTGGGTATATCTATTACA---GTGGGAGCACCAAC	174
QY	191	TACAAACCGCTCCCTCAAGAGTCGAGTCATCATTTTCAACAAGACACGTCACAAGAACAGTTC	250
Db	175	TACAAACCGCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCACAAGAACAGTTC	234
QY	251	TCCCTGAACTGAACTCTGTGTGACCGCGCGGACACGGCGGTGTATTACTGTGCCAGAGAT	310
Db	235	TCCCTGAACTGAGCTCTGTGACCGCTGCGGACACGGCGGTGTATTACTGTGCCAGAGG	294
QY	311	TGGGCCCA-----AATAGCTGGAACAACGCTAGCTCTCTGGGGCCAGGGAGTCTGTGTC	364
Db	295	GGGTACAGACTTTTGTACTGGTATGACTACTTGTACTCTGGGGCCAGGGAACCTGGTC	354
QY	365	ACCGTCTCCTCA	376
Db	355	ACCGTCTCCTCA	366

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RESULT 15
US-10-309-762-181
? Sequence 181, Application US/10309762
? Publication No. US20040018198A1
? GENERAL INFORMATION:
? APPLICANT: Gudas, Jean
? APPLICANT: Foltz, Ian
? APPLICANT: Banda, Masahisa
? APPLICANT: Gallo, Michael
? TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
? TITLE OF INVENTION: {CA IX} TUMOR ANTIGEN
? FILE REFERENCE: AGENIX.027A
? CURRENT APPLICATION NUMBER: US/10/309,762
? CURRENT FILING DATE: 2002-12-02
? PRIOR APPLICATION NUMBER: 60/337275
? PRIOR FILING DATE: 2001-12-03
? NUMBER OF SEQ ID NOS: 246
? SOFTWARE: PasSeq for Windows Version 4.0
? SEQ ID NO 181
? LENGTH: 367
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-309-762-181

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	Best Local Similarity	82.5%	Ref. No. 6.7e-63		
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DB	1	CRGTGCAGCTGCAGGAGTCGGGCCCAGAGCTGGTGAAGCCCTTCGGAGACCTGTGTCCCTC	60		
QY	71	ACCTGCGCTGTCTCTGGTGGCTCTGTGCAGCTAGTATACTGGTGGACCTGGATCGGCAG	130		
DB	61	ACCTGCACCTGTCTCTGGTGGCTC--CATCAGTAGTTACTACTGGAGCTGGATCGGCAG	117		
QY	131	CCCCCGGGAAGGACCTGGAGTGGATTGGAACGTATCTCTGGTGTGTTGGCGGCACCAAC	190		
DB	118	CCCCCGGAGGAGATGTGAGTGGATTGGTATATCTATTACA---GTGGGAGCACCAAC	174		
QY	191	TACAACCCGTCCTCAAGAGTCGAGTCATCATTTTCAACAAGACAGTCCCAAGACAGTTTC	250		
DB	175	TACAACCCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACAGCTCCAGAGACCGTTTC	234		

Qy	251	TCCCTGAACCTGAACCTCTGTGACCGCGGACAGCGCGGTATTTACTGTGCCAGAT	310
Db	235	TCCCTGAACCTGAACCTCTGTGACCGCGGACAGCGCGGTATTTACTGTGCCAGAT	294
Qy	311	TGGGCCCA-----AATAGCTGGAACACGCTAGGCTTCTGGGCGCAGGAGTCTGGTC	364
Db	295	GGGTACGACTTTTGTGACTGTTATGACTACTTTGACTACTGGGCGCAGGAAACCTGGTC	354
Qy	365	ACCGTCTCCTCA	376
Db	355	ACCGTCTCCTCA	366

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Job time : 285 secs

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 06:19:02 ; Search time 1733 Seconds
(without alignments)
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Title: US-09-019-441A-3_COPY_48_423
Perfect score: 376
Sequence: 1 ggtctgcccagctgcagc.....tcctgggtcacggtctctcca 376

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 13781830

Minimum DB seq length: 0
Maximum DB seq length: 376

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- EST:*
- 1: em_estba.*
 - 2: em_esthum.*
 - 3: em_estin.*
 - 4: em_estmu.*
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 - 6: em_estpl.*
 - 7: em_estro.*
 - 8: em_htc.*
 - 9: gb_est1.*
 - 10: gb_est2.*
 - 11: gb_htc.*
 - 12: gb_est3.*
 - 13: gb_est4.*
 - 14: gb_est5.*
 - 15: em_estfun.*
 - 16: em_estom.*
 - 17: em_gss_hum.*
 - 18: em_gss_inv.*
 - 19: em_gss_pln.*
 - 20: em_gss_vrt.*
 - 21: em_gss_fun.*
 - 22: em_gss_mam.*
 - 23: em_gss_mus.*
 - 24: em_gss_pro.*
 - 25: em_gss_rtd.*
 - 26: em_gss_pbg.*
 - 27: em_gss_vri.*
 - 28: gb_gss1.*
 - 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	228.4	60.7	374	10 AW403845	AW403845 UI-HF-BKO
2	224.6	59.7	319	10 AW405472	AW405472 UI-HF-BLO
3	218.8	58.2	369	10 AW404242	AW404242 UI-HF-BLO
4	217.8	57.9	370	10 AW402748	AW402748 UI-HF-BKO

5	217	57.7	367	10 AW403544	AW403544 UI-HF-BKO
6	216.8	57.7	353	10 AW401636	AW401636 UI-HF-BKO
7	215.2	57.2	363	10 AW403420	AW403420 UI-HF-BKO
8	212.8	56.6	368	10 AW403989	AW403989 UI-HF-BKO
9	208.6	55.5	358	12 BM820975	BM820975 K-EST0089
10	208.4	55.4	374	10 AW732986	AW732986 bbl8e10.Y
11	207.6	55.2	365	12 B1225611	B1225611 602948938
12	207.2	55.1	340	10 AWS03526	AWS03526 UI-HF-BNO
13	207	55.1	361	10 BF767440	BF767440 CMI-CN006
14	206.6	54.9	347	14 CD704336	CD704336 EST20863
15	204.8	54.5	342	10 AW733058	AW733058 bbl20e05.Y
16	204.2	54.3	345	10 BE167630	BE167630 CMO-HT050
17	204.2	54.3	357	12 BP432480	BP432480 BP432480
18	202.2	53.8	310	10 AW401919	AW401919 UI-HF-BKO
19	199.2	52.7	347	10 BF711155	BF711155 MRL-ET014
20	189.4	50.4	275	10 AW408669	AW408669 UI-HF-BMO
21	183.8	48.9	347	10 BF711157	BF711157 MRL-ET014
22	183.2	48.7	354	10 BE932781	BE932781 CMI-HT086
23	177.4	47.2	273	10 BF847860	BF847860 ILS-EN008
24	177.4	47.2	360	12 BM851875	BM851875 K-EST0132
25	175.6	46.7	368	10 AW842075	AW842075 RCO-CN002
26	175.4	46.6	270	10 BF869898	BF869898 MRL-ET014
27	173.6	46.2	342	12 BM851855	BM851855 K-EST0132
28	172.2	45.8	360	10 BF173443	BF173443 MYE1430a
29	171	45.5	246	12 B1059470	B1059470 PM4-UT010
30	171	45.5	246	12 B1061844	B1061844 PM4-UT010
31	170.6	45.4	345	14 CD695048	CD695048 EST11571
32	169.2	45.0	258	9 AA360195	AA360195 EST69374
33	169	44.9	279	10 AW403538	AW403538 UI-HF-BKO
34	168.8	44.9	240	12 EG950423	EG950423 CM3-CT060
35	168.8	44.9	327	10 AW361882	AW361882 PM3-CT026
36	168.4	44.8	337	10 AW869764	AW869764 MRL-SN007
37	168	44.7	248	10 AW403144	AW403144 UI-HF-BKO
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39	166.6	44.3	306	10 BF174894	BF174894 MYE4006.M
40	165.6	44.0	331	14 T27715	T27715 EST13381.Hu
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42	164.6	43.8	368	10 BF759686	BF759686 CMI-CT060
43	162	43.1	337	10 BF869893	BF869893 MRL-ET014
44	161.4	42.9	356	10 AW403007	AW403007 UI-HF-BKO
45	159	42.3	287	12 BG999993	BG999993 MR3-HN006

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
UI-HF-BKO-abl-h-02-0-UI-ri NIH_MGC_36 Homo sapiens cdna clone
IMAGE:3056859 5', mRNA sequence.
ACCESSION
AW403845
VERSION
AW403845.1 GI:6922998
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 374)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Rco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cdNA Library Preparation: M.B. Soares Lab
cdNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

Seq primer: M13 Forward.

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1. .319
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3061658"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 37"
/note="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 59.7%; Score 224.6; DB 10; Length 319;
Best Local Similarity 88.4%; Pred. No. 5.5e-48;
Matches 288; Conservative 0; Mismatches 29; Indels 6; Gaps 2;
QY 7 GTCCAGCTGCAGCTGCAGAGTCGGGCCAGAGGTGTAAGCCCTCGAGACCTGTC 66
Db 6 GGGCCAGGTGCAGCTGCAGAGTCGGGCCAGAGCTGGTGAAGCCCTCGAGACCTGTC 65
QY 67 CTTCCCTGGCTCTCTGGTGGCTCTGTGACAGTGTGATTAATCTGTCGACCTGGATCCG 126
Db 66 CTTCCCTGGCTCTCTGGTGGCTCTGTGACAGTGTGATTAATCTGTCGACCTGGATCCG 122
QY 127 CCAGCCCCCAGGAGGAGCTGGAGTGGAGTGTGACATCTCTGTTAGTGGTGGCCAC 186
Db 123 GCAGCCCCCAGGAGGAGCTGGAGTGGAGTGTGATTAATCTGTCGACCTGGATCCG 179
QY 187 CAATACACCCCTCCCTCAAGAGTGTGATTAATCTCTGTTAGTGGTGGCCAC 246
Db 180 CAATACACCCCTCCCTCAAGAGTGTGATTAATCTCTGTTAGTGGTGGCCAC 239
QY 247 GTTCTCCCTGAACCTCAACTCTGTGACCGCCGAGACAGCCGCTGTTACTGTGCCAG 306
Db 240 GTTCTCCCTGAACCTCAACTCTGTGACCGCCGAGACAGCCGCTGTTACTGTGCCAG 299
QY 307 AGA 309
Db 300 ACA 302

RESULT 3
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LOCUS
DEFINITION
UI-HF-BL0-adh-f-09-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3057545 5', mRNA sequence.
ACCESSION
AW404242
VERSION
AW404242.1 GI:6923299
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 369)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

FEATURES
source
1. .374
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:3061658"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 36"
/note="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 60.7%; Score 228.4; DB 10; Length 374;
Best Local Similarity 86.8%; Pred. No. 6.1e-49;
Matches 276; Conservative 0; Mismatches 36; Indels 6; Gaps 2;
QY 1 GGTCTGTCCAGCTGCAGCTGCAGAGTCGGGCCAGAGTGTGAGCCCTCGAGAC 60
Db 26 GGTCTGTCCAGCTGCAGCTGCAGAGTCGGGCCAGAGTGTGAGCCCTCGAGAC 85
QY 61 CTTGCTCTACCTGGCTGTCTGTGGTCTGTGACAGTGTGATTAATCTGTCGATGG 117
Db 86 CTTGCTCTACCTGGCTGTCTGTGGTCTGTGACAGTGTGATTAATCTGTCGATGG 145
QY 118 CTGATCCCGCAGCCCCCAGGAGGAGTGGAGTGGAGTGTGATTAATCTGTCGATGG 177
Db 146 CTGATCCCGCAGCCCCCAGGAGGAGTGGAGTGGAGTGTGATTAATCTGTCGATGG 202
QY 178 TGGGCCCCACCACTACACCCGCTCCCTCAAGAGTGTGATTAATCTGTCGATGG 237
Db 203 TGGGCCCCACCACTACACCCGCTCCCTCAAGAGTGTGATTAATCTGTCGATGG 262
QY 238 CAAGAACAGTCTCTCCCTGAACCTCAACTCTGTGACCGCCGAGACAGCCGCTGATTA 297
Db 263 CAAGAACAGTCTCTCCCTGAACCTCAACTCTGTGACCGCCGAGACAGCCGCTGATTA 322
QY 298 CTGTGCCAGAGTTGGC 315
Db 323 CTGTGCCAGAGTTGGC 340

RESULT 2
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LOCUS
DEFINITION
UI-HF-BL0-adh-d-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3061658 5', mRNA sequence.
ACCESSION
AW405472
VERSION
AW405472.1 GI:6924529
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 319)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
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 /cell_type="germinal center B cells"
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 /lab_host="DH10B (LT1)"
 /clone_lib="NIH_MGC_36"
 /note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 57.7%; Score 217; DB 10; Length 367;
 Best Local Similarity 83.1%; Pred. No. 5.7e-46;
 Matches 296; Conservative 0; Mismatches 51; Indels 9; Gaps 4;
 QY 10 CCAGCTGAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCT 69
 DB 18 CCAGTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCACAGACCTGTCCT 77
 QY 70 CACCTGGCTGTCTCTGTGGTCTGTGTGAGCA---GTAGTAAGTGGTGGACCTGGATCCG 126
 DB 78 CACCTGGACTGTCTCTGTGGTCTCCATCAGCAGTGGTAGTTACTACTGGAGCTGGATCCG 137
 QY 127 CAGCCCCCAGGAGGAGCTGAGTGGATGGAGCTATCTCTGTAGTGGTGGGCCAC 186
 DB 138 CAGGCCCGCGGGAAGGAGCTGGAGTGGATGGGGTATCT---ATAATAGTGGAGGAC 194
 QY 187 CAATCTACAAACCGTCCCTCAAGTTCGAGTATCATATTTCAAGACACAGTCCAGAACCA 246
 DB 195 CGACTACAAATTTCTCTCTCAAGTTCGACTCACCATATCAGTAGACAGTCCAGAACCA 254
 QY 247 GTTCTCCCTGAACCTGAACTGTGACCGCCGCGGACAGCGCGGTGTTACTGTGCCAG 306
 DB 255 GTTCTCCCTGAGCTGACCTGTGTGACCGCCGACAGACAGCGCGGTGTTACTGTGGAG 314
 QY 307 AGATTGGGCGCCAAATAGCTGGAACACGCTAGGCTTCTGGGCGCAGGAGTCTCTGG 362
 DB 315 AGGACGTATC--AACAGCTGGTAC-TTATTGACTACTGGGCGCAGGAAACCTTGG 367

RESULT 6

AW401636 353 bp mRNA linear EST 16-FEB-2000
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 IMAGE:3053596 5', mRNA sequence.
 ACCESSION AW401636
 VERSION AW401636.1 GI:6920322
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 353)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="IMAGE:3053596"
 /tissue_type="lymph"
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 /lab_host="DH10B (LT1)"
 /clone_lib="NIH_MGC_36"
 /note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 57.7%; Score 216.8; DB 10; Length 353;
 Best Local Similarity 86.0%; Pred. No. 6.3e-46;
 Matches 265; Conservative 0; Mismatches 37; Indels 6; Gaps 2;
 QY 1 GGTCTGTCTCCAGCTGCAGCTGCAGAGTCCGGCCAGGAGTGGTGAAGCTTCGGAGAC 60
 DB 29 GGTCTGTCTCCAGCTGCAGCTGCAGAGTGGGGCGGAGGACTGTTGAAGCTTCGGAGAC 88
 QY 61 CTTGTCCCTCACCTGGCTGTCTCTGGTGGCTCTGTTCAGCAGTAGTAAGTGGGACCTG 120
 DB 89 CTTGTCCCTCACCTGGCTGTCTCTATGTTGGGTC---CTTCAGTGTCTTACTACTGGAGCTG 145
 QY 121 GATCCGCCAGCCCCCAGGGAAGGAGCTGGAGTGGATTTGGACGCTATCTCTGTTAGTGTGG 180
 DB 146 GATCCGCCAGCCCCCAGGGAAGGAGTGGAGTGGATTTGGGAATCAATCATAGTGGAG 205
 QY 181 GGGCCACCACTACAACCCGTCCTCAAGAGTCGAGTCATCTTCATTTCAACAGACGTCCTCA 240
 DB 206 ---CACCAGTACAACCCGTCCTCAAGAGTCCAGTCCATATCATCATAGTACACGTCCTCA 262
 QY 241 GATCCAGTTCCTCCCTGAAGCTGACCTGTGACCGCGGCGGACACGCGCCCTGTATTACTG 300
 DB 263 GATCCAGTTCCTCCCTGAAGCTGAGCTCTGTACCGCCGCGGACACGCGCTGTATTACTG 322
 QY 301 TGGCAGAG 308
 DB 323 TGGCAGAG 330

RESULT 7

AW403420 363 bp mRNA linear EST 16-FEB-2000
 LOCUS
 DEFINITION UI-HF-BKO-abe-g-03-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
 IMAGE:3056068 5', mRNA sequence.
 ACCESSION AW403420
 VERSION AW403420.1 GI:6922356
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 363)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward
 Location/Qualifiers
 1..363
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 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 36"
 /notes="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 57.2%; Score 215.2; DB 10; Length 363;
 Best Local Similarity 85.4%; Pred. No. 1.7e-45;
 Matches 264; Conservative 0; Mismatches 39; Indels 6; Gaps 2;
 QY 1 GGTCTGTCCAGCTGCAGCTGCAGAGTCCGCCAGAGTGGTGAAGCTTCGAGAC 60
 Db 9 GGTCTGTCCAGCTGCAGCTGCAGAGTCCGCCAGAGTGGTGAAGCTTCAGAC 68
 QY 61 CCTGTCCCTCAGCTGCAGCTGCAGAGTCCGCCAGAGTGGTGAAGCTTCGAGAC 117
 Db 69 CCTGTCCCTCAGCTGCAGCTGCAGAGTCCGCCAGAGTGGTGAAGCTTCAGAC 128
 QY 118 CTGGATCCGCGCAGCTGCAGAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGG 177
 Db 129 CTGGATCCGCGCAGCTGCAGAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGG 185
 QY 178 TGGGGCCACCACTACAGCCCTCCCTCAGAGTCCAGTGCATCATTTTCACAGACGCTC 237
 Db 186 TGGAGGGCTACTACATCCGCTCCCTCAGAGTCCAGTGCATCATTTTCAGTACGACGCTC 245
 QY 238 CAAGAACCACTTCTCCCTGACCTGAACTCTGTGACCGCGCGGACACGCCCTGTATT 297
 Db 246 TAAGAACCACTTCTCCCTGAACTGAACTCTGTGACCTGCGCGGACACGCCCTGTATT 305
 QY 298 CTGTGCCAG 306
 Db 306 CTGTGTGAG 314

RESULT 8
 AW403989
 LOCUS
 DEFINITION UI-HF-BK0-abl-d-08-0-UI-ri NIH MGC_36 Homo sapiens cDNA clone
 IMAGE:3056679 5', mRNA sequence.
 AW403989
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 368)
 NIH-MGC <http://imgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward
 Location/Qualifiers
 1..368
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 36"
 /notes="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 56.6%; Score 212.8; DB 10; Length 368;
 Best Local Similarity 84.6%; Pred. No. 7.1e-45;
 Matches 264; Conservative 0; Mismatches 42; Indels 6; Gaps 2;
 QY 1 GGTCTGTCCAGCTGCAGCTGCAGAGTCCGCCAGAGTGGTGAAGCTTCGAGAC 60
 Db 42 GGTCTGTCCAGCTGCAGCTGCAGAGTCCGCCAGAGTGGTGAAGCTTCAGAC 101
 QY 61 CCTGTCCCTCAGCTGCAGCTGCAGAGTCCGCCAGAGTGGTGAAGCTTCGAGAC 117
 Db 102 CCTGTCCCTCAGCTGCAGCTGCAGAGTCCGCCAGAGTGGTGAAGCTTCAGAC 161
 QY 118 CTGGATCCGCGCAGCTGCAGAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGG 177
 Db 162 CTGGATCCGCGCAGCTGCAGAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGG 218
 QY 178 TGGGGCCACCACTACAGCCCTCCCTCAGAGTCCAGTGCATCATTTTCACAGACGCTC 237
 Db 219 TGGAGGGCTACTACATCCGCTCCCTCAGAGTCCAGTGCATCATTTTCAGTACGACGCTC 278
 QY 238 CAAGAACCACTTCTCCCTGACCTGAACTCTGTGACCGCGCGGACACGCCCTGTATT 297
 Db 279 TAAGAACCACTTCTCCCTGAGGCTGGTCTGTGACTGCGCGGACACGCCCTGTATT 338
 QY 298 CTGTGCCAG 309
 Db 339 CTGTGCCAG 350

RESULT 9
 BM820975
 LOCUS
 DEFINITION X-EST0089670 S19N665307 Homo sapiens cDNA clone S19N665307-9-C09
 5', mRNA sequence.
 BM820975
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 358)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 9 row: C column: 09
High quality sequence stop: 358.
Location/Qualifiers
1..358

FEATURES

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1..358
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="S19N65307-9-C09"
/sex="M"
/lab_host="Top10F"
/clone_lib="S19N65307"

/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 55.5%; Score 208.6; DB 12; Length 358;
Best Local Similarity 83.9%; Pred. No. 8.7e-44;
Matches 261; Conservative 0; Mismatches 44; Indels 6; Gaps 2;

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QY 1 GGTCTCTCCAGCTGCAGAGTGGGCCCCAGGAGTGTGAAGCTTCGGAGAC 60
DB 33 GGTCTCTCCAGTGCAGAGTGGGCCCCAGGAGTGTGAAGCTTCGGAGAC 92
QY 61 CTGTCTCTCCAGTGCAGAGTGGGCCCCAGGAGTGTGAAGCTTCGGAGAC 117
DB 93 CTGTCTCTCCAGTGCAGAGTGGGCCCCAGGAGTGTGAAGCTTCGGAGAC 152
QY 118 CTGTCTCTCCAGTGCAGAGTGGGCCCCAGGAGTGTGAAGCTTCGGAGAC 177
DB 153 CTGTCTCTCCAGTGCAGAGTGGGCCCCAGGAGTGTGAAGCTTCGGAGAC 209
QY 178 TGGGGCCACCACTACAACCCGTCCTCAAGAGTCGAGTCATCATTTCAAGACACGTC 237
DB 210 TGGGAGCATCAACTACAATACCTCCCTCAAGATCGAGTCACCATATCAATAGACCGTC 269
QY 238 CAAGAACCACTTCCTCCAGCTGACCTGTGACCGCGCGGAGACCGCGGTATTATTA 297
DB 270 CAAGATCACTTCCTCCAGTGAACCTGTGACCGCGCGGAGACCGCGGTATTATTA 329
QY 298 CTGTGCCAGAG 308
DB 330 CTGTGCTCGAG 340
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RESULT 10

AW732986
LOCUS
DEFINITION
bb18e10.y1 NIH MGC 8 Homo sapiens cDNA clone IMAGE:2963274 5' similar to gb:M54911.rnal IG HEAVY CHAIN PRECURSOR V-II REGION (HUMAN); mRNA sequence.
ACCESSION
VERSION
AW732986.1 GI:7633328
KEYWORDS
EST.

SOURCE

Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (Bases 1 to 374)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: sgabs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at:
image.lilnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 334.
Location/Qualifiers
1..374

FEATURES

source
1..374
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2963274"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 8"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.4%; Score 208.4; DB 10; Length 374;
Best Local Similarity 84.6%; Pred. No. 1e-43;
Matches 259; Conservative 0; Mismatches 41; Indels 6; Gaps 2;

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QY 61 CTGTCTCTCCAGTGCAGAGTGGGCCCCAGGAGTGTGAAGCTTCGGAGAC 120
DB 135 CTGTCTCTCCAGTGCAGAGTGGGCCCCAGGAGTGTGAAGCTTCGGAGAC 191
QY 121 GATCGGCCAGCCCCCAGGAGAGGAGTGGAGTGGATCTCTGTAGTGGTGG 180
DB 192 GATCGGCCAGCCCCCAGGAGAGGAGTGGAGTGGATCTCTGTAGTGGAG 251
QY 181 GGCACCAACTACACCGCTCCCTCAAGAGTCGAGTCATCATTTCAAGACACGTC 240
DB 252 ---CACCAACTACACCGCTCCCTCAAGAGTCGAGTCATCATTTCAAGACACGTC 308
QY 241 GAACCACTTCCTCCAGTGAACCTGTGACCGCGCGGAGACCGCGGTATTATCTG 300
DB 309 GAAGCAGCTCTCCCTGAGTTGAGCTCTGTGACCGCGCGGAGACCGCGGTATTATCTG 369
QY 301 TGGCAG 306
DB 369 TGGCAG 374
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RESULT 11

BI225611
LOCUS
DEFINITION
602948938F1 NIH MGC 8 Homo sapiens cDNA clone IMAGE:5093504 5', mRNA sequence.
ACCESSION
BI225611

VERSION BI225611.1 GI:14679055
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 365)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LICM1860 row: k column: 09
 High quality sequence stop: 365.
 Location/Qualifiers
 1. 365
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5093504"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_8"
 /note="Organ: lymph; Vector: pOT87; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 ORIGIN
 Query Match 55.2%; Score 207.6; DB 12; Length 365;
 Best Local Similarity 83.9%; Pred. No. 1.6e-43;
 Matches 260; Conservative 0; Mismatches 44; Indels 6; Gaps 2;
 QY 1 GGTCTCTCCAGCTGCAGCTGAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 60
 Db 55 GGTCTCTCCAGCTGCAGCTGAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 114
 QY 61 CCTCTCCTCAGCTGCGCTGTCTCTGTGGCTCTGTGACAGTAGTAACTGGTGGACCTG 120
 Db 115 CCTCTCCTCAGCTGCGCTGTCTGTGGCTCTGTGACAGTAGTAACTGGTGGACCTG 171
 QY 121 GATCCGCGACCCCGGAGGAGCTGGAGTGGATTCGACGTATCTCTGTGGTGGTGG 180
 Db 172 GATCCGCGACCCCGGAGGAGCTGGAGTGGATTCGACGTATCTCTGTGGTGGTGG 231
 QY 181 GGCACCAACTACAAACCGCTCCCTCAAGAGTGCAGTCAATCATTTCAAGACACGCTCA 240
 Db 232 ---CAACCACTACAAACCGCTCCCTCAAGAGTGCAGTCAATCATTTCAAGACACGCTCA 288
 QY 241 GAACAGTTCTCCCTGAACCTGAACCTGTGACCGCGCGGACACGCGCTGTATTACTG 300
 Db 289 GAACAGTTCTCCCTGAAGTTGAGCTCTGTGAACGCGCGGACACGCGCTGTATTACTG 348
 QY 301 TGCCAGAGAT 310
 Db 349 TGCAGAGATT 358
 RESULT 12
 AW503526
 LOCUS
 DEFINITION UI-HP-BN0-aky-b-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
 340 bp mRNA linear EST 01-MAR-2000
 AW503526
 LOCUS
 DEFINITION UI-HP-BN0-aky-b-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone

IMAGE:3078487 5', mRNA sequence.
 AW503526
 VERSION AW503526.1 GI:7140086
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 340)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.
 Location/Qualifiers
 1. 340
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3078487"
 /tissue_type="lymph"
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 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH_MGC_50"
 /note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (3.5-4.4kb). Directionally cloned. Cells provided by
 Louis M. Staudt, Ph.D. Library preparation by Maria de
 Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
 ORIGIN
 Query Match 55.1%; Score 207.2; DB 10; Length 340;
 Best Local Similarity 84.1%; Pred. No. 2e-43;
 Matches 259; Conservative 0; Mismatches 43; Indels 6; Gaps 2;
 QY 1 GGTCTCTCCAGCTGCAGCTGAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 60
 Db 32 GGTCTCTCCAGCTGCAGCTGAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 91
 QY 61 CCTGTCCCTCAGCTGCGCTGTCTCTGTGGCTCTGTGACAGTAG---TAACCTGGTGGAC 117
 Db 92 CCTGTCCCTCAGCTGCAGCTGCGCTGTCTGTGGCTCTGTGACAGTAGTCTTACTTGGGG 151
 QY 118 CTGGATCCGCGACCCCGGAGGAGCTGGAGTGGATTCGACGTATCTCTGTGGTGG 177
 Db 152 CTGGATCCGCGACCCCGGAGGAGCTGGAGTGGATTCGACGTATCTTATTA---C 208
 QY 178 TGGGGCCACCAACTACAAACCGCTCCCTCAAGAGTGCAGTCAATTTCAAGACACGCTC 237
 Db 209 TGGACCACTACTACACACCGCTCCCTCCAGAGTGCAGTCAATATCGTTGACACGCGC 268
 QY 238 CAAGAACAGTTCTCTCTGAACCTGAACCTGTGTGACCGCGCGGACACGCGCTGTATTAT 297
 Db 269 CAAGAACAGTTCTCTCTGGATCTGAGCTCAGTACCGCGCGGACACGCGCTTATTATTA 328
 QY 298 CTGTGCCA 305
 Db 329 TTGTGCGA 336
 RESULT 13
 BF767440
 LOCUS
 DEFINITION BF767440 361 bp mRNA linear EST 12-JAN-2001

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DEFINITION CM1-CN0061-131200-642-c02 CN0061 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF767440
VERSION BF767440.1 GI:12115340
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 361)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Sucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,P., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ci=CM1&t2=CM1-CN0061-
131200-642-c02&t3=2000-12-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 360.
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Location/Qualifiers
1..361
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CN0061"
/note="Organ: colon normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 55.1%; Score 207; DB 10; Length 361;
Best Local Similarity 86.6%; Pred. No. 2.3e-43;
Matches 252; Conservative 0; Mismatches 35; Indels 4; Gaps 2;
QY 1 GGTCTGTCCAGCTGCAGCTGCAGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGAC 60
Db 74 GGTCTGTCTCAGGTGCAGCTGCAGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGAC 133
QY 61 CTTGTCTCTACCTCGCTGTCTCTGTGGTGGCTCTGTGACGAGTAGTACTGTGGACCTG 120
Db 134 CTTGTCTCTACCTCGCTGTCTCTGTGGTGGCTCTGTGACGAGTAGTACTGTGGAGTTG 193
QY 121 GATCC-GCCAGCCCCCAGGAGGACTGGAGTGGATTGGACGTATCTCTGCTAGTGGTG 179
Db 194 GGTCTGTGCGCCCCCAGGAGGGGCTGGAGTGGATTGGGAAATCATCATATA---GTG 250
QY 180 GGGCCACCAACTACAAACCCGCTCCCTCAAGAGTGCAGTGCATCATTTTCAAGACACGTCCTCA 239
Db 251 GGAGCACCACCACTTCAACCCGCTCCCTCAAGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 310
QY 240 AGAACCACTTCTCCCTGAACTGAACTCTGTGACCGCGCGGACACGCGCG 290
Db 311 AGAACCACTTCTCCCTGAACTGAACTCTGTGACCGCGCGGACACGCGCG 361
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RESULT 14
LOCUS CD704336
DEFINITION EST20863 human nasopharynx Homo sapiens cDNA, mRNA linear EST 25-JUN-2003
ACCESSION CD704336
VERSION CD704336.1 GI:32234966
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 347)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsums.edu.cn.
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Location/Qualifiers
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library from southern Chinese"
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Best Local Similarity 86.6%; Pred. No. 2.9e-43;
Matches 240; Conservative 0; Mismatches 34; Indels 3; Gaps 1;
QY 1 GGTCTGTCTCCAGCTGCAGCTGCAGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGAC 60
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Db 134 CTTGTCTCTACCTCGCTGTCTCTGTGGTGGCTCTGTGACGAGTAGTACTGTGGAGTTG 193
QY 121 GATCCGCCAGCCCCCAGGAGGACTGGAGTGGATTGGACGTATCTCTGCTAGTGGTG 180
Db 194 GGTCTGTGCGCCCCCAGGAGGGGCTGGAGTGGATTGGGAAATCTTACCACA---GTGG 250
QY 181 GGGCCACCAACTACAAACCCGCTCCCTCAAGAGTGCAGTGCATCATTTTCAAGACACGTCCTCA 240
Db 251 GAGCACCACCACTACAAACCCGCTCCCTCAAGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 310
QY 241 GAACCACTTCTCCCTGAACTGAACTCTGTGACCGCG 277
Db 311 GAACCACTTCTCCCTGAACTGAACTCTGTGACCGCG 347
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LOCUS AW733058
DEFINITION bb20805.Y1 NIH MGC 8 Homo sapiens cDNA clone IMAGE:2963456 5',
similar to gb:M54911.mal IG HEAVY CHAIN PRECURSOR V-II REGION
(HUMAN);, mRNA sequence.
ACCESSION AW733058
VERSION AW733058.1 GI:7633401
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Search completed: June 19, 2004, 07:31:24
Job time : 1737 secs

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 04:01:44 ; Search time 1844 Seconds
(without alignments)
7545.073 Million cell updates/sec

Title: US-09-019-441a-5_COPY_67_387
Perfect score: 321
Sequence: 1 gacatccagatgacccagtc.....ggaccaaggaggaaatcaaa 321

Scoring table: IDENTITY NUC
Gapop 10.0 , Gabext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 2865150

Minimum DB seq length: 0
Maximum DB seq length: 321

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.or.*
- 21: em.ov.*
- 22: em.pat.*
- 23: em.ph.*
- 24: em.pl.*
- 25: em.ro.*
- 26: em.sts.*
- 27: em.un.*
- 28: em.vi.*
- 29: em.htg.hum.*
- 30: em.htg.inv.*
- 31: em.htg.pln.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rat.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sv.*
- 39: em.hgo.hum.*
- 40: em.hgo.mus.*
- 41: em.hgo.other.*

Pred. No. is the number of results predicted by chance to have a

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2	279.4	87.0	321	9	AY240164	AY240164 Homo sapi
3	273.2	85.1	311	9	HSA243111	AJ243111 Homo sapi
4	271.4	84.5	320	9	AF329459	AF329459 Homo sapi
5	271	84.4	320	9	HSA0408420	AJ408420 Homo sapi
6	270.4	84.2	313	9	AY062340	AY062340 Homo sapi
7	270	84.1	318	9	AF103418	AF103418 Homo sapi
8	269.8	84.0	321	9	AF090357	AF090357 Homo sapi
9	269.8	84.0	321	9	AF090357	L26035 Homo sapien
10	269.6	84.0	318	12	AF044451	AF044451 Synthetic
11	269.6	84.0	321	6	AR160973	AR160973 Sequence
12	269.6	84.0	321	6	AR161046	AR161046 Sequence
13	269.6	84.0	321	6	AR161049	AR161049 Sequence
14	269.6	84.0	321	6	AR161050	AR161050 Sequence
15	269.4	83.9	320	9	HSA0408417	AJ408417 Homo sapi
16	268.2	83.6	321	9	AY240163	AY240163 Homo sapi
17	268	83.5	318	12	AF044454	AF044454 Synthetic
18	268	83.5	321	6	AR160976	AR160976 Sequence
19	266.8	83.1	319	9	AF103383	AF103383 Homo sapi
20	266.6	83.1	315	6	A68531	A68531 Sequence 47
21	266.6	83.1	315	9	HSLD217VL	Y08249 H.sapiens m
22	266.6	83.1	321	6	AX354835	AX354835 Sequence
23	266.6	83.1	321	9	AF442762	AF442762 Homo sapi
24	266.6	83.1	321	9	HSSIA15VL	Z46311 H.sapiens i
25	266.4	83.0	318	12	AF044456	AF044456 Synthetic
26	266.4	83.0	321	6	AR160978	AR160978 Sequence
27	266.4	83.0	321	6	AR161044	AR161044 Sequence
28	265	82.6	314	9	AY062338	AY062338 Homo sapi
29	265	82.6	321	9	AY240165	AY240165 Homo sapi
30	264.8	82.5	318	12	AF044447	AF044447 Synthetic
31	264.8	82.5	318	12	AF044453	AF044453 Synthetic
32	264.8	82.5	321	6	AR160969	AR160969 Sequence
33	264.8	82.5	321	6	AR160975	AR160975 Sequence
34	264.8	82.5	321	6	AR161035	AR161035 Sequence
35	264.2	82.3	311	9	HSX98988	X98988 H.sapiens r
36	264	82.2	313	9	AY082339	AY082339 Homo sapi
37	264	82.2	321	12	AY315905	AY315905 Synthetic
38	263.4	82.1	321	6	E12913	E12913 Human cDNA
39	263.4	82.1	321	6	AX522255	AX522255 Sequence
40	262.8	81.9	318	9	AF306388	AF306388 Homo sapi
41	261.8	81.6	315	6	A68499	A68499 Sequence 15
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43	261.8	81.6	321	6	A29589	A29589 H.sapiens c
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ALIGNMENTS

RESULT 1
HSA0408402
LOCUS HSA0408402 320 bp DNA linear PRI 01-AUG-2001
DEFINITION Homo sapiens partial IGKV gene for immunoglobulin kappa chain
variable region, clone 7.
ACCESSION AJ408402
VERSION AJ408402.1 GI:12655491
KEYWORDS IGKV gene; immunoglobulin kappa chain; immunoglobulin light chain;
variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 320)
AUTHORS Harfist,E., Cooper,S., Neubauer,S., Distel,L. and Grawunder,U.

TITLE Normal V(D)J recombination in cells from patients with Nijmegen
breakage syndrome
JOURNAL Mol. Immunol. 37 (15), 915-929 (2000)
MEDLINE 21179652
PUBMED 11282395
REFERENCE 2 (bases 1 to 320)
AUTHORS Harfst, E.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-2001) Harfst E., Immunologie,
Universitätsklinikum Ulm, Albert-Einstein-Allee 115 D-89081 Ulm,
GERMANY

FEATURES
source Location/Qualifiers
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Best Local Similarity 92.5%; Pred. No. 6.2e-79;
Matches 295; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 3 CATTCAGATGACCCAGTCTCCATCTTCCTGTCATCTGTAGGGGACAGATCACCAT 62
DB 1 CATTCAGATGACCCAGTCTCCATCTTCCTGTCATCTGTAGGAGACAGATCACCAT 60
QY 63 CATTCGACGGCAGTCAGGACATAGGTATTTAAATTTGTATCAGCAGAACCCAGG 122
DB 61 CATTTGCGGCGCAGTCAGGCGATTAGAAATGATTTAGGCTGGTATCAGCAGAACCCAGG 120
QY 123 AAGAGCTCTAGCTCTGATCTATGTTGCATCCAGTTTGCAGAGTGGGTCCTCATCAAG 182
DB 121 GAAAGCCCTAAGCGCCCTGATCTATGCTGCATCCAGTTTGCAGAGTGGGTCCTCATCAAG 180
QY 183 GTTCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCCAGCTCAGCAGCCCTGCAGCCTGA 242
DB 181 GTTCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCCAGCTCAGCAGCCCTGCAGCCTGA 240
QY 243 AGATTTTGGACTTATTAATCTGTCACAGTTTATAGTACCCCTCGGAGTTTCGGCCAGG 302
DB 241 AGATTTTGCACCTTATTAATCTGTCACAGTTTATAGTACCCCTCGGAGTTTCGGCCAGG 300
QY 303 GACCAAGGTGGAAATCAAA 321
DB 301 GACCAAGGTGGAAATCAAA 319

RESULT 2
AY240164
LOCUS
DEFINITION Homo sapiens clone HA6 anti-HAV capsid immunoglobulin G light chain
variable region mRNA, partial cds.
ACCESSION AY240164

VERSION AY240164.1 GI:29650334
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 321)
AUTHORS Kim, S.J., Jang, M.H., Stapleton, J.T., Yoon, S.O., Jeon, E.-S. and
Hong, H.J.
TITLE Neutralizing Human Monoclonal Antibodies to Hepatitis A Virus
Recovered by Phage Display
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 321)
AUTHORS Kim, S.J., Jang, M.H., Stapleton, J.T., Yoon, S.O., Jeon, E.-S. and
Hong, H.J.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2003) Antibody Engineering RU, Korea Research
Institute of Bioscience and Biotechnology, Yuseung, Daejeon 305-333,
Korea
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/clone="HA6"
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variable region"
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Best Local Similarity 91.9%; Pred. No. 1.5e-78;
Matches 295; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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DB 1 GACATTCAGATGACCCAGTCTCCATCTTCCTGTCATCTGTAGGAGACAGATCACC 60
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QY 181 AGGTTTCAGCGCAGTGGATCTGGGACAGAGTTTCACTCTCAGCTCAGCAGCCTGCAGCCT 240
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QY 301 GGGACCAAGGTGAAATCAAA 321
DB 301 GGGACCAAGGTGAAATCAAA 321

RESULT 3
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LOCUS
DEFINITION Homo sapiens partial mRNA for immunoglobulin light chain variable
region (a30 gene).
ACCESSION AJ243111
VERSION AJ243111.1 GI:5102680
KEYWORDS a30 gene; immunoglobulin light chain; variable region.

RESULT 5
HSA408420 320 bp DNA linear PRI 01-AUG-2001
LOCUS
DEFINITION Homo sapiens partial IGKV gene for immunoglobulin kappa chain
variable region, clone 25.
ACCESSION
VERSION AJ408420.1 GI:12655525
KEYWORDS IGKV gene; immunoglobulin kappa chain; immunoglobulin light chain;
variable region.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Harfst, E., Cooper, S., Neubauer, S., Distel, L. and Grawunder, U.
TITLE Normal V(D)J recombination in cells from patients with Nijmegen
breakage syndrome
JOURNAL Mol. Immunol. 37 (15), 915-929 (2000)
MEDLINE 21179652
PUBMED 11282395
REFERENCE
AUTHORS Harfst, E.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-2001) Harfst E., Immunologie,
Universitaetsklinikum Ulm, Albert-Einstein-Allee 115 D-89081 Ulm,
GERMANY
FEATURES
source Location/Qualifiers
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Query Match 84.4%; Score 271; DB 9; Length 320;
Best Local Similarity 90.6%; Pred. No. 7.7e-76;
Matches 289; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 3 CATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACCAT 62
DB 1 CATCCAGTGGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACCAT 60
QY 63 CACTTCAGGCGCAGTGGATCTGGACAGATTCTATTTAAATTTGGTATCGATCAGCAAAACCCAG 122
DB 61 CACTTCGCGGCGCAGTGGATCTGGACAGATTCTATTTAGCTGATTCAGCAAAACCCAG 120
QY 123 AAAAGCTCTTAAGCTCTGATCTATGTCATCCAGTTTGCAAAAGTGGGTCCTCCATCAAG 182
DB 121 GAAAGCCCTAAGCTCTGATCTATGCTGCTGCTCCATTTGCAAAAGTGGGTCCTCCATCAAG 180
QY 183 GTTCAGGCGCAGTGGATCTGGACAGATTCTCTACCCGTCAGACGCTCGACGCTGA 242
DB 181 GTTCAGGCGCAGTGGATCTGGACAGATTCTCTCAATCAACAGCTCGACGCTGA 240

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DB 241 AGATTTTGGAGTCTATTACTGCTACAGGTTATAGTACCCCTCGGAGCTTCGGCAAG 300
QY 303 GACCAAGGTGGAAATCAAA 321
DB 301 GACCAAGGTGGAAATCAAA 319
RESULT 6
AY062340 313 bp mRNA linear PRI 23-JAN-2002
LOCUS
DEFINITION Homo sapiens clone 59/707 immunoglobulin light chain kappa variable
region mRNA, partial cds.
ACCESSION
VERSION AY062340
KEYWORDS
SOURCE AY062340.1 GI:18307283
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Vaisbourd, M., Ignatovich, O., Dremcheva, A., Karpas, A. and Winter, G.
TITLE Molecular characterization of human monoclonal antibodies derived
from fusions of tonsil lymphocytes with a human myeloma cell line
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 313)
AUTHORS Vaisbourd, M., Ignatovich, O., Dremcheva, A., Karpas, A. and Winter, G.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2001) MRC Laboratory of Molecular Biology, Hills
Road, Cambridge CB2 2QH, UK
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source Location/Qualifiers
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KVEIK"
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Query Match 84.2%; Score 270.4; DB 9; Length 313;
Best Local Similarity 91.7%; Pred. No. 1.2e-75;
Matches 286; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 10 ATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACCATCTTGC 69
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QY 130 CCTAAGCTCTGATCTATGTTGTCATCCAGTTTGCATAGTGGGTCCCATCAAGTTTCA 189
DB 121 CCTAAGCTCTGATCTATGCTGTCATCCAGTTTGCATAGTGGGTCCCATCAAGTTTCA 180
QY 190 GGCAGTGGATCTGGACAGAGTTCACCTCTCAGCTGAGCCCTGCGAGCTTGAGATTTT 249
DB 181 GGCAGTGGATCTGGACAGAGTTCACCTCTCAGCTGAGCCCTGCGAGCTTGAGATTTT 240
QY 250 GCGATTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGCTTCGGCCCAAGGACCA 309
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Db 181 CAGTGGATCTGGCACAGATTTCACCTCACCATCAGCAGCCTGACGCTGAAGATTTTGC 240

QY 252 GACTTATTACTGTCTACAGGTTTANAGTACCCCTCGACGTTTGGCCAGGACCAAGGT 311

Db 241 AACTTATTACTGTCTACAGGTTTACATTTACCTCGACGTTTGGCCAGGACCAAGGT 300

QY 312 GGAATCAAA 321

Db 301 GGAATCAAA 310

RESULT 8

AF090357 321 bp mRNA linear PRI 24-SEP-1998

LOCUS Homo sapiens clone G8 anti-mucini light chain variable region mRNA,

DEFINITION partial cds.

ACCESSION AF090357

VERSION AF090357.1 GI:3644021

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 321)

AUTHORS Andersson, E., Henderikx, P., Krambovitis, E., Hoogenboom, H.R. and Borrebaeck, C.A.K.

TITLE A tandem repeat of MUC1 core protein induces a weak in vitro immune response in human B cells

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 321)

AUTHORS Andersson, E., Henderikx, P., Krambovitis, E., Hoogenboom, H.R. and Borrebaeck, C.A.K.

TITLE Direct Submission

JOURNAL Submitted (04-SEP-1998) Immunotechnology, Lund University, P.O. Box 7031, Lund 220 07, Sweden

FEATURES

source Location/Qualifiers

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/organism="Homo sapiens"

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ORIGIN

Query Match 84.0%; Score 269.8; DB 9; Length 321;

Best Local Similarity 90.0%; Pred. No. 1.9e-75;

Matches 289; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 GACATCCAGATGACCCAGTCTCCATCTCTGCTGTCATCTGTAGGAGCAGATGACC 60

Db 1 GACATCCAGATGACCCAGTCTCCATCTCTGCTGTCATCTGTAGGAGCAGATGACC 60

QY 61 ATCACTTCGCGGCGAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 120

Db 61 ATCACTTCGCGGCGAGTCAGGACATTAGGTATTATTTGGTATCAGCAGAAACCA 120

QY 121 GGAAGAGTCTCTAAGCTCTCTGATCTATGTCATCCAGTTTGCAGTGGGTCCTCATCA 180

Db 121 GGAAGAGTCTCTAAGCTCTCTGATCTATGTCATCCAGTTTGCAGTGGGTCCTCATCA 180

QY 181 AGTTTCAGGCGAGTGGATCTGGGACAGATTTCACTCTCAGCTCAGCAGCTGCGAGCT 240

Db 181 AGTTTCAGGCGAGTGGATTTGGGACAGATTTCACTCTCAGCTCAGCAGCTGCGAGCT 240

QY 310 GTGGAATCAAA 321

Db 301 GTGGAATCAAA 312

RESULT 7

AF103418 318 bp mRNA linear PRI 03-MAR-1999

LOCUS Homo sapiens isolate donor D clone D79K immunoglobulin kappa light

DEFINITION chain variable region mRNA, partial cds.

ACCESSION AF103418

VERSION AF103418.1 GI:4323899

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 318)

AUTHORS de Wildt, R.M., Hoet, R.M., van Venrooij, W.J., Tomlinson, I.M. and Winter, G.

TITLE Analysis of heavy and light chain pairings indicates that receptor editing shapes the human antibody repertoire

JOURNAL J. Mol. Biol. 285 (3), 895-901 (1999)

MEDLINE 99141350

PUBMED 9887257

REFERENCE 2 (bases 1 to 318)

AUTHORS de Wildt, R.M.T., Hoet, R.M.A., van Venrooij, W.J., Tomlinson, I.M. and Winter, G.

TITLE Direct Submission

JOURNAL Submitted (29-OCT-1998) Centre for Protein Engineering, MRC, Hills Road, Cambridge CB2 2QH, UK

FEATURES

source Location/Qualifiers

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QY 72 GGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCAAGCTCC 131

Db 61 GGCAAGTCAGGACATTAGGTATTAGGCTGGTATCAGCAGAAACCAAGAGCCCC 120

QY 132 TAAGCTCTGATCTATGTCATCCAGTTTGAAGTGGGTCCTCATCAGGTTCAAGCG 191

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QY 241 GAAGATTTTGGCACTTATTAGTCTCAGAGTTTATAGTACCCCTCGAGCTTCGGCCAA 300
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QY 301 GGGACCAAGTGGGAATCAAA 321
Db 301 GGGACCAAGTGGGAATCAAA 321

RESULT 9
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LOCUS
DEFINITION Homo sapiens immunoglobulin Igm light chain variable region mRNA,
partial cds.
ACCESSION L26035
VERSION L26035.1 GI:415710
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 321)
AUTHORS Azmi, F.H., Lucas, A.H., Raff, H.V. and Granoff, D.M.
TITLE Variable region sequences and idiotypic expression of a protective
human immunoglobulin M antibody to capsular polysaccharides of
Neisseria meningitidis group B and Escherichia coli K1
JOURNAL Infect. Immun. 62 (5), 1776-1786 (1994)
MEDLINE 94222544
PUBMED 8168940
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Matches 289; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Db 301 GGGACCAAGTGGGAATCAAA 321

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LOCUS
DEFINITION Synthetic construct from Homo sapiens clone 102 anti-Rh(D) antibody
V kappa segment mRNA, partial cds.
ACCESSION AF044451
VERSION AF044451.1 GI:3046473
KEYWORDS
SOURCE Synthetic construct
ORGANISM Synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 318)
AUTHORS Siegel, D.L., Chang, T.Y., Russell, S.L. and Bunya, V.Y.
TITLE Isolation of cell surface-specific human monoclonal antibodies
using phage display and magnetically-activated cell sorting:
applications in immunohematology
J. Immunol. Methods 206 (1-2), 73-85 (1997)
MEDLINE 97469098
PUBMED 9328570
REFERENCE
2 (bases 1 to 318)
AUTHORS Chang, T.Y. and Siegel, D.L.
TITLE Genetic and immunological properties of phage-displayed human
anti-Rh(D) antibodies: implications for Rh(D) epitope topology
JOURNAL Blood 91 (8), 3066-3078 (1998)
MEDLINE 98200617
PUBMED 9531621
REFERENCE
3 (bases 1 to 318)
AUTHORS Chang, T.Y., Russell, S.L., Bunya, V.Y. and Siegel, D.L.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1998) Path & Lab Med, University of Pennsylvania,
36th & Hamilton, Philadelphia, PA 19104, USA
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Best Local Similarity 90.8%; Pred. No. 2.2e-75;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 6 CCAGTACCCAGTCTCCATCTCCCTGCTCGATCTGTAGGGGACAGAGTCACCATCAC 65
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QY 66 TTGCAGGCGAAGTCAGACATAGTATTATTTAAATTTGGTATCAGCAGAAACAGGAAA 125
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QY 243 AGATTTTGGCACTTATTACTGCTACAGGTTTATAGTACCCCTCGGACGTTGCGCAAGG 302
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QY 303 GACCAAGGTGGAAATCAAA 321
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Db 301 GACCAAGGTGGAAATCAAA 319
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Search completed: June 19, 2004, 05:12:10
Job time : 1846 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 03:30:47 ; Search time 276 Seconds
(without alignments)

4940.839 Million cell updates/sec

Title: US-09-019-441a-5_COPY_67_387

Perfect score: 321

Sequence: 1 Gacatccagatgaccagtc.....ggaccgaagtggaaatcaa 321

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 4121650

Minimum DB seq length: 0
Maximum DB seq length: 321

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: Geneseqn2000s:*
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8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	269.6	84.0	321	5	AAH68720 Human ant
2	269.6	84.0	321	5	AAH68723 Human ant
3	269.6	84.0	321	5	AAH68647 Human ant
4	269.6	84.0	321	5	AAH68724 Human ant
5	269.6	84.0	321	8	ACD45311 Anti-Rh(D
6	269.6	84.0	321	8	ACD45384 Anti-Rh(D
7	269.6	84.0	321	8	ACD45388 Anti-Rh(D
8	269.6	84.0	321	8	ACD45387 Anti-Rh(D
9	268.2	83.6	321	7	ABZ24183 Anti-EGFR
10	268	83.5	321	5	AAH68650 Human ant
11	268	83.5	321	5	AAH68652 Human ant
12	266.6	83.1	315	2	AAV19759 Antibody
13	266.6	83.0	321	6	ABA06023 Human mon
14	266.4	83.0	321	5	AAH68718 Human ant
15	266.4	83.0	321	5	AAH68652 Human ant
16	266.4	83.0	321	8	ACD45382 Anti-Rh(D
17	266.4	83.0	321	8	ACD45316 Anti-Rh(D
18	264.8	82.5	321	5	AAH68649 Human ant
19	264.8	82.5	321	5	AAH68643 Human ant
20	264.8	82.5	321	5	AAH68709 Human ant
21	264.8	82.5	321	8	ACD45307 Anti-Rh(D
22	264.8	82.5	321	8	ACD45313 Anti-Rh(D
23	264.8	82.5	321	8	ACD45373 Anti-Rh(D

24	263.4	82.1	321	2	AAT66781	Anti-canc
25	263.4	82.1	321	6	ABS52471	Human DNA
26	261.8	81.6	315	2	AAV19743	Antibody
27	261.8	81.6	321	4	AAH47731	Nucleotid
28	261.8	81.6	321	4	AAH47735	Nucleotid
29	261.6	81.5	321	5	AAH68717	Human ant
30	261.6	81.5	321	5	AAH68719	Human ant
31	261.6	81.5	321	5	AAH68703	Human ant
32	261.6	81.5	321	8	ACD45367	Anti-Rh(D
33	261.6	81.5	321	8	ACD45383	Anti-Rh(D
34	261.6	81.5	321	8	ACD45381	Anti-Rh(D
35	260.2	81.1	315	2	AAV19757	Antibody
36	260.2	81.1	315	2	AAV19761	Antibody
37	260.2	81.1	321	6	AAH45899	Human end
38	260.2	81.1	321	6	ABA94337	MAb #3 11
39	260	81.0	321	5	AAH68713	Human ant
40	258.4	80.5	318	2	AAH68745	Antibody
41	258.4	80.5	321	5	AAH68654	Human ant
42	258.4	80.5	321	5	AAH68701	Human ant
43	258.4	80.5	321	5	AAH68701	Human ant
44	258.4	80.5	321	8	ACD45318	Anti-Rh(D
45	258.4	80.5	321	8	ACD45365	Anti-Rh(D

ALIGNMENTS

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AAH68720
ID AAH68720 standard; DNA; 321 BP.

AC AAH68720;

DT 14-SEP-2001 (first entry)

XX Human anti-Rh(D) antibody clone SH49 nucleotide sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

XX red blood cell; Rh phenotype; diagnosis; therapeutic; ds.

XX Homo sapiens.

XX US6255455-B1.

XX 03-JUL-2001.

XX 29-JAN-1999; 99US-00240274.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-0089404S.

XX 10-APR-1998; 98US-0081380P.

XX (TYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

XX WPI; 2001-388931/41.

XX P-PSDB; AAG93663.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in diagnostics requiring a human instead of an animal antibody and in therapeutic medicine.

XX Example 3; Col 79; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein, preferably a human antibody, (I) having an amino acid sequence comprising one of the sequences (S) given in AAG93558 to AAG93669. (I) has immunostimulant activity, and can be used as an immune system stimulant. (I) can be used in diagnostic and therapeutic medicine. The antibodies are used in diagnostics that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood cells. AAH68615 to AAH68726 represent the nucleotide sequence which encode


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XX PN US2003040605-A1.
XX PD 27-FEB-2003.
XX PF 04-MAY-2001; 2001US-00848798.
XX PR 11-OCT-1996; 96US-0028550P.
XX PR 27-JUN-1997; 97US-00884045.
XX PR 10-APR-1998; 98US-0081380P.
XX PR 29-JAN-1999; 99US-00240274.
XX PA (UTYPE-) UNIV PENNSYLVANIA.
XX PI Siegel DL;
XX DR WPI; 2003-512273/48.
XX DR P-PSDB; ABO27397.
XX PT New human Rh(D)-binding protein useful for various diagnostic and
XX PT therapeutic applications, including typing of blood or blood products.
XX PS Claim 12; Page 39; 187pp; English.
XX PS The invention relates to an isolated Rh(D) binding protein. The protein
XX CC can be used for magnetically activated cell sorting. The protein is
XX CC useful in various diagnostic and therapeutic applications in humans,
XX CC including typing of blood or blood products. The present sequence
XX CC represents DNA encoding a human anti-Rh(D) chain
XX SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;

Query Match      84.0%; Score 269.6; DB 8; Length 321;
Best Local Similarity 90.8%; Pred. No. 1.1e-78;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTCCCTGTCGATCTCTAGGGGACAGAGTCACCATCAC 65
DB 3 CGAGCTCACCCAGTCTCCATCTCCCTGTCGATCTCTAGGGGACAGAGTCACCATCAC 62
QY 66 TTGCGGGCAGTCAGGACGATTTAGTATTATTAAATGGTATCAGCAGAAACAGGAAA 125
DB 63 TTGCGGGCAGTCAGGACGATTTAGTATTATTAAATGGTATCAGCAGAAACAGGAAA 122
QY 126 AGCTCTTAAGCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTT 185
DB 123 AGCCCTTAAGCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTT 182
QY 186 CAGCGGACGTGATCTGGGACAGAGTTCACTCTCAGCGTCAGCAGCCTGAGCTGAGA 245
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DB 303 CAAGTGGAAATCAAA 318

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XX AC ACD45384;
XX DT 12-SEP-2003 (first entry)
XX DE Anti-Rh(D) light chain SH49 DNA.
XX KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
XX magnetically activated cell sorting.

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XX OS Homo sapiens.
XX PN US2003040605-A1.
XX PD 27-FEB-2003.
XX PF 04-MAY-2001; 2001US-00848798.
XX PR 11-OCT-1996; 96US-0028550P.
XX PR 27-JUN-1997; 97US-00884045.
XX PR 10-APR-1998; 98US-0081380P.
XX PR 29-JAN-1999; 99US-00240274.
XX PA (UTYPE-) UNIV PENNSYLVANIA.
XX PI Siegel DL;
XX DR WPI; 2003-512273/48.
XX DR P-PSDB; ABO27470.
XX PT New human Rh(D)-binding protein useful for various diagnostic and
XX PT therapeutic applications, including typing of blood or blood products.
XX PS Claim 12; Page 61; 187pp; English.
XX PS The invention relates to an isolated Rh(D) binding protein. The protein
XX CC can be used for magnetically activated cell sorting. The protein is
XX CC useful in various diagnostic and therapeutic applications in humans,
XX CC including typing of blood or blood products. The present sequence
XX CC represents DNA encoding a human anti-Rh(D) chain
XX SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;

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Best Local Similarity 90.8%; Pred. No. 1.1e-78;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTCCCTGTCGATCTCTAGGGGACAGAGTCACCATCAC 65
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DB 63 TTGCGGGCAGTCAGGACGATTTAGTATTATTAAATGGTATCAGCAGAAACAGGAAA 122
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DB 183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAGCGTCAGCAGCCTGAGCTGAGA 242
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DB 303 CAAGTGGAAATCAAA 318

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XX AC ACD45388;
XX DT 12-SEP-2003 (first entry)
XX DE Anti-Rh(D) light chain SH54 DNA.
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KW Human; ds; gene; RH(D) binding protein; blood typing; blood product; magnetically activated cell sorting;
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OS Homo sapiens.
XX US2003040605-A1.
XX 27-FEB-2003.
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XX 04-MAY-2001; 2001US-00848798.
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XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX 29-JAN-1999; 99US-00240274.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Siegel DL;
XX WPI; 2003-512273/48.
XX P-PSDB; ABO27474.
XX
XX New human Rh(D)-binding protein useful for various diagnostic and therapeutic applications, including typing of blood or blood products.
XX
XX Claim 12; Page 61; 187pp; English.
XX
XX The invention relates to an isolated Rh(D) binding protein. The protein can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents DNA encoding a human anti-Rh(D) chain
XX
SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
Query Match 84.0%; Score 269.6; DB 8; Length 321;
Best Local Similarity 90.8%; Pred. No. 1.1e-78;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 5 CCAGATGACCCAGTCTCCATCTTCCCTGCTGATCTGTAGGGACAGAGTCACCATCAC 65
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Db 303 CAGGTTGGAAATCAAA 318
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AC ACD45387;
XX
DT 12-SEP-2003 (first entry)
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DE Anti-Rh(D) light chain SH52 DNA.
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KW Human; ds; gene; RH(D) binding protein; blood typing; blood product; magnetically activated cell sorting.
XX
OS Homo sapiens.
XX US2003040605-A1.
XX 27-FEB-2003.
XX
XX 04-MAY-2001; 2001US-00848798.
XX
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX 29-JAN-1999; 99US-00240274.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Siegel DL;
XX WPI; 2003-512273/48.
XX P-PSDB; ABO27473.
XX
XX New human Rh(D)-binding protein useful for various diagnostic and therapeutic applications, including typing of blood or blood products.
XX
XX Claim 12; Page 61; 187pp; English.
XX
XX The invention relates to an isolated Rh(D) binding protein. The protein can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents DNA encoding a human anti-Rh(D) chain
XX
SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
Query Match 84.0%; Score 269.6; DB 8; Length 321;
Best Local Similarity 90.8%; Pred. No. 1.1e-78;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 5 CCAGATGACCCAGTCTCCATCTTCCCTGCTGATCTGTAGGGACAGAGTCACCATCAC 65
Db 3 CGAGTCAACCCAGTCTCCATCTTCCCTGCTGATCTGTAGGGACAGAGTCACCATCAC 62
QY 66 TTGCAGGGCAAGTCAGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAAGGAA 125
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Db 303 CAGGTTGGAAATCAAA 318
RESULT 9
ABZ24183
ID ABZ24183 standard; cDNA; 321 BP.
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AC ABZ24183;
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DT 14-APR-2003 (first entry)
XX Anti-EGFR antibody 2F8 VL chain encoding DNA.
DE Monoclonal antibody; Mab; 2F8; human; epidermal growth factor receptor;
XX EGFR; immunoglobulin; cytostatic; immunosuppressive; antiinflammatory;
KW antiarthritic; antipsoriatic; gene; ds.
XX Homo sapiens.
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FT /product= "VL chain"
FT /note= "the start and stop codons are not indicated"
XX WO2002100348-A2.
XX
XX 19-DEC-2002.
XX 13-JUN-2002; 2002WO-US018748.
XX 13-JUN-2001; 2001US-0298172P.
XX (GENM-) GENMAB AS.
XX (MEDA-) MEDAREX INC.
XX Van De Winkel J, Van Dijk MA, Gerritsen AF, Halk E;
XX WPI; 2003-167368/16.
XX P-PSDB; ASB82945.
XX Novel isolated human monoclonal antibody which binds to human epidermal
XX growth factor receptor, useful for treating or preventing a disease
XX mediated by expression of epidermal growth factor receptor such as
XX cancer.
XX
XX Disclosure; Pig 15A; 117pp; English.
XX
XX The invention relates to an isolated human monoclonal antibody (Mab)
XX which binds to human epidermal growth factor receptor (EGFR), where the
XX Mab is selected from immunoglobulin (IgG1, IgA, IgE, IgM, IgG4 and IgD
XX antibodies. The Mab is useful for inhibiting growth of a cell expressing
XX EGFR, for inducing cytotoxicity of a cell expressing EGFR, or for detecting
XX the presence of EGFR antigen, or a cell expressing EGFR. It is useful for
XX treating or preventing a disease mediated by expression of EGFR, where
XX the disease is cancer (such as bladder, breast, colon, kidney, ovarian,
XX prostate, renal, or head and neck cancer), or an autoimmune disease (such
XX as inflammatory arthritis), where the autoimmune disease involves
XX epithelial hyperproliferation. The Mab can be conjugated to a binding
XX specificity for a FC receptor or to a cytotoxin. It is useful as
XX diagnostic or therapeutic agents in vivo and in vitro for EGFR-related
XX diseases, for inhibiting growth and/or mediating phagocytosis and killing
XX of cells expressing EGFR, for treating autoimmune disease such as
XX psoriasis, to opsonize a cell expressing EGFR, to mediate phagocytosis or
XX cytotoxicity of a cell expressing EGFR in the presence of human effector
XX cells, to inhibit EGFR or TGF-alpha induced autophosphorylation of EGFR,
XX to target cells expressing Fc gammaR or EGFR, for example for labeling
XX such cells, or for detecting the presence of or quantifying the amount of
XX FC-expressing cells in vivo or in vitro. The present sequence represents
XX a DNA encoding the VL chain of an anti-EGFR antibody 2F8
XX
XX Sequence 321 BP; 81 A; 85 C; 77 G; 78 T; 0 U; 0 Other;
SQ

Db 61 ATCACTTGGCGGCAAGTCAGACATTAGCAGTGCTTTAGTCTGATCAGCAACCA 120
Qy 121 GGAAGAGCTCTAAGCTTCCTGATCTATGTCATCCAGTTTGCAGAGTGGGTCCCATCA 180
Db 121 GGAAGAGCTCTAAGCTTCCTGATCTATGTCATCCAGTTTGCAGAGTGGGTCCCATCA 180
Qy 181 AGGTTTCAGCGGCGAGTGGATCTGGGACAGAGTTTCACTCTCACCCTCAGCAGCCTGCAGCCT 240
Db 181 AGGTTTCAGCGGCGAGTGGATCTGGGACAGAGTTTCACTCTCACCCTCAGCAGCCTGCAGCCT 240
Qy 241 GAAGATTTTCGGACTTATTTACTGTCTACAGTTTATAGTACCCCTGGAGCTTGGGCCAA 300
Db 241 GAAGATTTTCGGACTTATTTACTGTCTACAGTTTATAGTACCCCTGGAGCTTGGGCCAA 300
Qy 301 GGGACCAAGGTGGAAATCAAA 321
Db 301 GGGACCAAGGTGGAGATCAAA 321
RESULT 10
AAH68650
ID AAH68650 standard; DNA; 321 BP.
XX AC AAH68650;
XX DT 14-SEP-2001 (first entry)
XX DE Human anti-Rh(D) chain I05 nucleotide sequence.
XX KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX OS Homo sapiens.
XX XX US6255455-B1.
XX PD 03-JUL-2001.
XX PF 29-JAN-1999; 99US-00240274.
XX PR 11-OCT-1996; 96US-0028550P.
XX PR 27-JUN-1997; 97US-00884045.
XX PR 10-APR-1998; 98US-0081380P.
XX PA (UYPE-) UNIV PENNSYLVANIA.
XX PI Siegel DL;
XX DR WPI; 2001-388931/41.
XX DR P-PSDB; AAG93593.
XX PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
XX PT diagnostics requiring a human instead of an animal antibody and in
XX PS therapeutic medicine.
XX PS Example 2; Col 55; 162pp; English.
XX CC The present invention describes an isolated Rh(D) binding protein,
XX CC preferably a human antibody. (I) having an amino acid sequence comprising
XX CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX CC immunostimulant activity, and can be used as an immune system stimulant.
XX CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
XX CC are used in diagnostics that require human antibodies instead of animal
XX CC antibodies, such as to determine the Rh phenotype of human red blood cells.
XX CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
XX CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
XX CC chain CDR3 amino acid sequences which are given in the exemplification of
XX CC the present invention
XX SQ Sequence 321 BP; 87 A; 88 C; 73 G; 73 T; 0 U; 0 Other;
XX Query Match 83.5%; Score 268; DB 5; Length 321;

Best Local Similarity 90.5%; Pred. No. 3.9e-78;		
Matches 286;	Conservative 0;	Mismatches 30; Indels 0; Gaps 0;
6	CCAGATCACCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACCATCAC	65
DB		
3	CGAGCTCACCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC	62
66	TTGCAGGGCAAGTCAGGACCATTAGGTATTATTTAAATTGGTATCAGCAGAAACACGAGAA	125
DB		
63	TTGCCGGGCAAGTCAGAGCATTAGGAGGTATTTAAATTGGTATCAGCAGAAACACGAGAA	122
126	AGCTCCTTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGTT	185
DB		
123	AGCCCTTAAGCTCCTGATCTTTTCTGCAATCCAGTTTGCAAAGTGGGGTCCCATCAAGTT	182
186	CAGCGGCAGTGGATCTCGGACAGAGTTCACTCTCACCGTCACAGCCTTCGAGCCTCGAAGA	245
DB		
183	CAGTGGCAGTGGATCTCGGACAGATTTCACTCTCACCATCAGCAGTCTCGCAACCTCGAGA	242
246	TTTTTGGCACTTATTAATCTGTACAGGTTTATAGTACCCTCGAGCTTTCGGCCGAGGAC	305
DB		
243	TTTTTGCATCTTACTACTGTCAACAGAGTTACAGTACCCCTCAACAGTTTCGGCCGAGGAC	302
306	CAAGGTGGAAATCAAA	321
DB		
303	CAAGGTGGAAATCAAA	318

RESULT 11	
ACD45314	
ID ACD45314 standard; DNA; 321 BP.	
XX	
ACD45314;	
XX	
AC	
12-SEP-2003 (first entry)	
XX	
DT	
XX	
DE Anti-Rh(D) chain I05 DNA.	
XX	
Human; ds; gene; RH(D) binding protein; blood typing; blood product;	
KW magnetically activated cell sorting.	
XX	
OS	
XX Homo sapiens.	
XX	
PN US2003040605-A1.	
XX	
PD	
XX 27-FEB-2003.	
XX	
04-MAY-2001; 2001US-00848798.	
XX	
11-OCT-1996; 95US-0028550P.	
PR	
27-JUN-1997; 97US-00884045.	
PR	
10-APR-1998; 98US-0081380P.	
PR	
29-JAN-1999; 99US-00240274.	
PR	
XX	
PA (UYPE-) UNIV PENNSYLVANIA.	
XX	
XX	
PI Siegel DL;	
XX	
XX	
WPI: 2003-51273/48.	
DR	
DR P-PSDB; ABO27400.	
XX	
XX	
PT New human Rh(D)-binding protein useful for various diagnostic and	
PT therapeutic applications, including typing of blood or blood products.	
PS	
PS Claim 12: Page 40; 187pp; English.	

	Query Match	83.5%;	Score 268;	DB 8;	Length 321;
	Best Local Similarity	90.5%;	Pred. No. 3.9e-78;		
	Matches 286;	Conservative 0;	Mismatches 30;	Indels 0;	Gaps 0;
QY	6	CCAGATGACCCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGGACAGAGTCCACATCAC	65		
DB	3	CGAGTCTACCCAGTCTCCATCTCTCTGTCTGCATCTGTAGGACAGAGTCCCATCAC	62		
QY	66	TTGCAGGGCAAGTCAGGACATTAGGTATTTATTTAAATTTGGTTATCAGCAGAAACGAGAAA	125		
DB	63	TTGCGGGGCAAGTCAGAGCATTTAGGAGGTATTTAAATTTGGTTATCAGCACAACACGAGGAA	122		
QY	126	AGCTCTTAAGCTCCGTGATCTATGTGTGCATCCAGGTTTGCAAGTGGGGTCCCATCAAGGTT	185		
DB	123	AGCCCTTAAGCTCCGTGATCTTTGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTT	182		
QY	186	CAGCGCAGTGGATCTGGACACAGATTCATCTCAACGTCACAGCGCTCAGCGCTCAAGA	245		
DB	183	CACCTGCAGTGGATCTGGGACAGATTTCACTCTCAACATCAGCAGCTGCGAACCTGAAGA	242		
QY	246	TTTTTGGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTGGGCCAAGGGAC	305		
DB	243	TTTTTGGACTTACTGTCTCAAGAGTTTCAGTACCCCTCAAAACGTTGGGCCAAGGGAC	302		
QY	306	CAAGGTGGAAATCAAA	321		
DB	303	CAAGGTGGAAATCAAA	318		

RESULT 12
AAV19759
ID AAV19759 standard; DNA; 315 BP.
XX
XX
XX AAV19759;
XX
XX
XX DT DT (first entry)
XX
XX 12-JUN-1998
XX
XX Antibody LD2-17-VL chain coding sequence.
XX
XX Antbody; variable heavy chain; VH chain; variable light chain; VL chain;
KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW idiopathic thrombocytopenic purpura; haemolytic disease of the newborn;
KW ss.
XX
XX Homo sapiens.
XX OS
XX WO9749809-A1.
XX PN
XX
XX 31-DEC-1997.
XX PD
XX
XX 20-JUN-1997; 97WO-EP003253.
XX PF
XX
XX 24-JUN-1996; 96EP-00810421.
XX PR
XX
XX (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX PA
XX
XX Miescher S, Vogel M, Stadler B, Morell A, Imboden M, Amstutz H;
XX PI
XX WPI; 1998-077173/07.
XX DR
XX P-PSDS; AAM52235.
XX
XX New Rhesus D antigen binding polypeptide(s) - used to neutralise Rhesus
PT D antigen in therapy, e.g. for treating idiopathic thrombocytopenic
PT purpura.
XX
XX
XX Claim 6; Fig 12B; 68pp; English.
XX
XX This sequence encodes the antibody LD2-17-VL chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The

D6	63	TTGCGGCAAGTCAGACATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCCAGGAA	122
QY	126	AGCTCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAAGTGGGTCCCATCAAGTT	185
D6	123	AGCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGTT	182
QY	186	CAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCGAGCCTGAAGA	245
D6	183	CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA	242
QY	246	TTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTCGGCCBAGGAC	305
D6	243	TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCGAACTTTGCGCGAGGAC	302
QY	306	CAAGTGGAAATCAAA	321
D6	303	CAAGTGGAGATCAAA	318

Search completed: June 19, 2004, 04:41:18
Job time : 277 secs

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 04:31:48 ; Search time 64 Seconds
(without alignments)
2783.426 Million cell updates/sec

Title: US-09-019-441A-5_COPY_67_387
Perfect score: 321
Sequence: 1 gacatccagatgacccagtc.....ggaccaagtggaatacaaa 321

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 582709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 104408

Minimum DB seq length: 0
Maximum DB seq length: 321

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A-COMB.seq: *
2: /cgn2_6/prodata/2/ina/5B-COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A-COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B-COMB.seq: *
5: /cgn2_6/prodata/2/ina/PCFUS-COMB.seq: *
6: /cgn2_6/prodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	269.6	84.0	321	3	US-09-240-274-102
2	269.6	84.0	321	3	US-09-240-274-216
3	269.6	84.0	321	3	US-09-240-274-221
4	269.6	84.0	321	3	US-09-240-274-222
5	268	83.5	321	3	US-09-240-274-105
6	266.4	83.0	321	3	US-09-240-274-107
7	266.4	83.0	321	3	US-09-240-274-216
8	264.8	82.5	321	3	US-09-240-274-98
9	264.8	82.5	321	3	US-09-240-274-104
10	264.8	82.5	321	3	US-09-240-274-207
11	261.8	81.6	321	3	US-08-378-939-13
12	261.6	81.5	321	3	US-09-240-274-201
13	261.6	81.5	321	3	US-09-240-274-215
14	261.6	81.5	321	3	US-09-240-274-217
15	260	81.0	321	3	US-09-240-274-211
16	258.4	80.5	321	3	US-09-240-274-109
17	258.4	80.5	321	3	US-09-240-274-199
18	257	80.1	321	1	US-08-488-376-12
19	257	80.1	321	2	US-08-634-223-12
20	257	80.1	321	2	US-08-634-224-12
21	257	80.1	321	2	US-08-634-400-12
22	257	80.1	321	2	US-08-635-878-12
23	257	80.1	321	2	US-08-770-057-12
24	257	80.1	321	3	US-09-335-697B-12
25	257	80.1	321	4	US-09-335-697B-12
26	257	80.1	321	4	US-09-740-002-12
27	256.8	80.0	321	3	US-09-240-274-113

28	256.8	80.0	321	3	US-09-240-274-102
29	253.6	79.0	321	3	US-09-240-274-205
30	253.6	79.0	321	3	US-09-240-274-106
31	253.6	79.0	321	3	US-09-240-274-200
32	252	78.5	321	3	US-09-240-274-213
33	250.6	78.1	321	3	US-08-598-226-36
34	250.6	78.1	321	3	US-09-125-098-36
35	250.6	78.1	321	3	US-09-540-018-36
36	250.4	78.0	321	3	US-09-240-274-114
37	240.8	75.0	318	3	US-09-240-274-208
38	236.2	73.6	321	4	US-09-560-198A-5
39	234.6	73.1	321	1	US-07-988-430-74
40	234.6	73.1	321	1	US-08-425-336-72
41	234.6	73.1	321	1	US-08-488-113B-72
42	234.6	73.1	321	1	US-08-477-484B-72
43	234.6	73.1	321	1	US-08-472-788A-76
44	234.6	73.1	321	2	US-08-646-360-72
45	234.6	73.1	321	2	US-08-082-842A-76

ALIGNMENTS

RESULT 1
US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6253455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-102

Query Match Similarity 84.0%; Score 269.6; DB 3; Length 321;
Best Local Similarity 90.8%; Pred. No. 4.9e-81;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY	6	CCAGATGACCCAGTCTCCATCTTCCCTGCTGTGCATCTGTAGGGACAGAGTCACCATCAC	65
DB	3	CGAGCTACCCAGTCTCCATCTTCCCTGCTGTGCATCTGTAGGGACAGAGTCACCATCAC	62
QY	66	TTGAGGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCGAAACCAAGGAAA	125
DB	63	TTGCGGGCAAGTCAGGACATAGGAGCTATTTAAATTTGGTATCAGCGAAACCAAGGAAA	122
QY	126	AGTCTCTAAGCTCTCGATCTATTTGCATCCAGTTTGCAGTTGGGGTCCCATCAAGGTT	185
DB	123	AGCCCTAAGTCTCTGATCTATTTGCTGATCTCAGTTTGCAGTTGGGGTCCCATCAAGGTT	182
QY	186	CAGCGGACAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCGCTTCGACCTGAAGA	245
DB	183	CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA	242
QY	246	TTTTTGGCACTTATTAAGTCTTACAGGTTTATAGTACCCCTGGAGCTTCGGCCCAAGGAC	305
DB	243	TTTTTGAACCTTACTACTGTCAACAGAGTTTACAGTACCCCTGGAGCTTCGGCCCAAGGAC	302
QY	306	CAAGGTGGAATCAAA	321

Db 63 TTGCGGGCAAGTCAGACATGGCACTTATTTAAATGGTATCAGCGAAACACGGGAA 122
Qy 126 AGCTCCTAAGCTCCTGATCTAGTTGTCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTT 185
Db 123 AGCCCTAAGCTCCTGATCTATGTCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTT 182
Qy 186 CAGCGGCAAGTCAGACATGGCACTTCACTCTCAGCTCAGCAGCTTGCAGCCTGAAGA 245
Db 183 CAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCACCTGAAGA 242
Qy 246 TTTTGGCACTTATTAAGTCTACAGGTTTATAGTACCCCTCGGACGTTGGCCCAAGGAC 305
Db 243 TTTTGGCACTTATTAAGTCTACAGGTTTATAGTACCCCTCGGACGTTGGCCCAAGGAC 302
Qy 306 CAAGGTGGAATCAAA 321
Db 303 CAAGGTGGAATCAAA 318

RESULT 5
US-09-240-274-105
; Sequence 105, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 105
US-09-240-274-105
Query Match 83.5%; Score 268; DB 3; Length 321;
Best Local Similarity 90.5%; Pred. No. 1.7e-80;
Matches 286; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 6 CCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 65
Db 3 CGAGCTCACCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 62
Qy 66 TTGCGGGCAAGTCAGACATGGCACTTATTTAAATGGTATCAGCGAAACACGGGAA 125
Db 63 TTGCGGGCAAGTCAGACATGGCACTTATTTAAATGGTATCAGCGAAACACGGGAA 122
Qy 126 AGCTCCTAAGCTCCTGATCTAGTTGTCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTT 185
Db 123 AGCCCTAAGCTCCTGATCTATGTCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTT 182
Qy 186 CAGCGGCAAGTCAGACATGGCACTTCACTCTCAGCTCAGCAGCTTGCAGCCTGAAGA 245
Db 183 CAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCACCTGAAGA 242
Qy 246 TTTTGGCACTTATTAAGTCTACAGGTTTATAGTACCCCTCGGACGTTGGCCCAAGGAC 305
Db 243 TTTTGGCACTTATTAAGTCTACAGGTTTATAGTACCCCTCGGACGTTGGCCCAAGGAC 302
Qy 306 CAAGGTGGAATCAAA 321
Db 303 CAAGGTGGAATCAAA 318

RESULT 6
US-09-240-274-107
; Sequence 107, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 107
US-09-240-274-107
Query Match 83.0%; Score 266.4; DB 3; Length 321;
Best Local Similarity 90.2%; Pred. No. 5.9e-80;
Matches 285; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 6 CCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 65
Db 3 CGAGCTCACCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 62
Qy 66 TTGCGGGCAAGTCAGACATGGCACTTATTTAAATGGTATCAGCGAAACACGGGAA 125
Db 63 TTGCGGGCAAGTCAGACATGGCACTTATTTAAATGGTATCAGCGAAACACGGGAA 122
Qy 126 AGCTCCTAAGCTCCTGATCTAGTTGTCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTT 185
Db 123 AGCCCTAAGCTCCTGATCTATGTCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTT 182
Qy 186 CAGCGGCAAGTCAGACATGGCACTTCACTCTCAGCTCAGCAGCTTGCAGCCTGAAGA 245
Db 183 CAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCACCTGAAGA 242
Qy 246 TTTTGGCACTTATTAAGTCTACAGGTTTATAGTACCCCTCGGACGTTTCGGCCCAAGGAC 305
Db 243 TTTTGGCACTTATTAAGTCTACAGGTTTATAGTACCCCTCGGACGTTTCGGCCCAAGGAC 302
Qy 306 CAAGGTGGAATCAAA 321
Db 303 CAAGGTGGAATCAAA 318

RESULT 7
US-09-240-274-216
; Sequence 216, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
US-09-240-274-216
Query Match 83.5%; Score 268; DB 3; Length 321;
Best Local Similarity 90.5%; Pred. No. 1.7e-80;
Matches 286; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Sequence 207, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 207
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH28
US-09-240-274-207

Query Match 82.5%; Score 264.8; DB 3; Length 321;
Best Local Similarity 89.9%; Pred. No. 2e-79;
Matches 284; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 6 CCATGATGACCCAGTCTGATCTCCCTGCTGATCTGTAGGAGACAGAGTCAACATCAC 65
Db 3 CGAGCTCACCAGTCTCCATCTCCCTGCTGATCTGTAGGAGACAGAGTCAACATCAC 62
QY 66 TTGCGGGCAGATCAGACATAGGATATTATTTAAATGCTATCAGCAGAAACCGGAAA 125
Db 63 TTGCGGGCAGATCAGACATAGGAGTCTTTAAATGCTTTTCCAGCAGAAACCGGAAA 122
QY 126 AGCTCTTAAGTCTGATCTATGTTGATCAGTTTGCAAGTGGGGTCCCATCAAGTTT 185
Db 123 AGCCCTTAAGTCTGATCTATGTTGATCAGTTTGCAAGTGGGGTCCCATCAAGTTT 182
QY 186 CAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTCGAGCTCAAGA 245
Db 183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCACTGAGA 242
QY 246 TTTTGGCACTTACTCTCTAAGTTTATAGTACCCCTCGGAGCTTGGGCCAAGGGAC 305
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QY 306 CAAGTGGAAATCAA 321
Db 303 CAAGTGGAAATCAA 318

RESULT 11
US-08-378-939-13
Sequence 13, Application US/08378939
Patent No. 5876361
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: Both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..321
US-08-378-939-13

Query Match 81.6%; Score 261.8; DB 2; Length 321;
Best Local Similarity 88.5%; Pred. No. 2.1e-78;
Matches 284; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 GACATCAGATGACCCAGTCTCCATCTTCCTCTGTCATCTCTGAGGGACAGAGTCAAC 60
Db 1 GACATCAGATGACCCAGTCTCCATCTTCCTCTGTCATCTCTGAGGGACAGAGTCAAC 60
QY 61 ATCACTTTCAGGGCAGTCTGAGCAGATTTAGTATTTTAAATTTGGTATCAGCAGAAACCA 120
Db 61 ATCACTTTCAGGGCAGTCTGAGCAGATTTAGTATTTTAAATTTGGTATCAGCAGAAACCA 120
QY 121 GAAAAAGCTCTAAGTCTCTGATCTATGTTGTCATCAGATTTGCAAGTGGGGTCCCATCA 180
Db 121 GAAAAAGCTCTAAGTCTCTGATCTATGTTGTCATCAGATTTGCAAGTGGGGTCCCATCA 180
QY 181 AGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACCTCTCACCGTCAGCAGCTCGAGCCT 240
Db 181 AGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACCTCTCACCGTCAGCAGCTCGAGCCT 240
QY 241 GAGATTTTCGAGTCTTACTCTCTACAGTTTATAGTACCCCTCGAGCTTGGGCCAA 300
Db 241 GAGATTTTCGAGTCTTACTCTCTACAGTTTATAGTACCCCTCGAGCTTGGGCCAA 300
QY 301 GGGACCAAGGTGGAAATCAA 321
Db 301 GGGACCAAGGTGGAGATTAA 321

RESULT 12
US-09-240-274-201
Sequence 201, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224

Sequence 207, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 207
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH28
US-09-240-274-207

Query Match 82.5%; Score 264.8; DB 3; Length 321;
Best Local Similarity 89.9%; Pred. No. 2e-79;
Matches 284; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 6 CCATGATGACCCAGTCTGATCTCCCTGCTGATCTGTAGGAGACAGAGTCAACATCAC 65
Db 3 CGAGCTCACCAGTCTCCATCTCCCTGCTGATCTGTAGGAGACAGAGTCAACATCAC 62
QY 66 TTGCGGGCAGATCAGACATAGGATATTATTTAAATGCTATCAGCAGAAACCGGAAA 125
Db 63 TTGCGGGCAGATCAGACATAGGAGTCTTTAAATGCTTTTCCAGCAGAAACCGGAAA 122
QY 126 AGCTCTTAAGTCTGATCTATGTTGATCAGTTTGCAAGTGGGGTCCCATCAAGTTT 185
Db 123 AGCCCTTAAGTCTGATCTATGTTGATCAGTTTGCAAGTGGGGTCCCATCAAGTTT 182
QY 186 CAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTCGAGCTCAAGA 245
Db 183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCACTGAGA 242
QY 246 TTTTGGCACTTACTCTCTAAGTTTATAGTACCCCTCGGAGCTTGGGCCAAGGGAC 305
Db 243 TTTTGGCACTTACTCTCTAAGTTTATAGTACCCCTCGGAGCTTGGGCCAAGGGAC 302
QY 306 CAAGTGGAAATCAA 321
Db 303 CAAGTGGAAATCAA 318

RESULT 11
US-08-378-939-13
Sequence 13, Application US/08378939
Patent No. 5876361
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: Both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..321
US-08-378-939-13

Query Match 81.6%; Score 261.8; DB 2; Length 321;
Best Local Similarity 88.5%; Pred. No. 2.1e-78;
Matches 284; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 GACATCAGATGACCCAGTCTCCATCTTCCTCTGTCATCTCTGAGGGACAGAGTCAAC 60
Db 1 GACATCAGATGACCCAGTCTCCATCTTCCTCTGTCATCTCTGAGGGACAGAGTCAAC 60
QY 61 ATCACTTTCAGGGCAGTCTGAGCAGATTTAGTATTTTAAATTTGGTATCAGCAGAAACCA 120
Db 61 ATCACTTTCAGGGCAGTCTGAGCAGATTTAGTATTTTAAATTTGGTATCAGCAGAAACCA 120
QY 121 GAAAAAGCTCTAAGTCTCTGATCTATGTTGTCATCAGATTTGCAAGTGGGGTCCCATCA 180
Db 121 GAAAAAGCTCTAAGTCTCTGATCTATGTTGTCATCAGATTTGCAAGTGGGGTCCCATCA 180
QY 181 AGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACCTCTCACCGTCAGCAGCTCGAGCCT 240
Db 181 AGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACCTCTCACCGTCAGCAGCTCGAGCCT 240
QY 241 GAGATTTTCGAGTCTTACTCTCTACAGTTTATAGTACCCCTCGAGCTTGGGCCAA 300
Db 241 GAGATTTTCGAGTCTTACTCTCTACAGTTTATAGTACCCCTCGAGCTTGGGCCAA 300
QY 301 GGGACCAAGGTGGAAATCAA 321
Db 301 GGGACCAAGGTGGAGATTAA 321

RESULT 12
US-09-240-274-201
Sequence 201, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 201
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-240-274-201

Query Match 81.5%; Score 261.6; DB 3; Length 321;
Best Local Similarity 89.2%; Pred. No. 2.4e-78;
Matches 282; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACATCAC 65
DB 3 CGAGTCAACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACATCAC 62

QY 66 TTGCGAGGCAAGTCAAGATAGTATTTAAATTTGGTATCAGCAGAAACCCAGGAA 125
DB 63 TTGCGGGCAAGTCAAGATAGTATTTAAATTTGGTATCAGCAGAAACCCAGGAA 122

QY 126 AGCTCTTAAGTCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTT 185
DB 123 AGCCCTTAAGTCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTT 182

QY 186 CAGCGGCAAGTCTGAGTCTGGGACAGAGTTCATCTCAGCTTCAGCAGCCTGAGCTCAAGA 245
DB 183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAGCAGTCTGCAACCTGAAGA 242

QY 246 TTTTGGCACTTATTACTGTCTCAGAGTTTATAGTACCCCTCGGACGTTTCGGCCCAAGGAC 305
DB 243 TTTTGGCACTTACTACTGTCTCAGAGTTCATCTCAGCAGTTCAGCTTCCCTAGCACTTTGGCCCTGGAC 302

QY 306 CAAGTGGAAATCAAA 321
DB 303 CAAGTGGATATCAAA 318

RESULT 14
US-09-240-274-217
Sequence 217, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 217
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH48
US-09-240-274-217

Query Match 81.5%; Score 261.6; DB 3; Length 321;
Best Local Similarity 89.2%; Pred. No. 2.4e-78;
Matches 282; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACATCAC 65
DB 3 CGAGTCAACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACATCAC 62

QY 66 TTGCGAGGCAAGTCAAGATAGTATTTAAATTTGGTATCAGCAGAAACCCAGGAA 125
DB 63 TTGCGGGCAAGTCAAGATAGTATTTAAATTTGGTATCAGCAGAAACCCAGGAA 122

QY 126 AGCTCTTAAGTCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTT 185
DB 123 AGCCCTTAAGTCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTT 182

QY 186 CAGCGGCAAGTCTGAGTCTGGGACAGAGTTCATCTCAGCTTCAGCAGCCTGAGCTCAAGA 245
DB 183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAGCAGTCTGCAACCTGAAGA 242

QY 246 TTTTGGCACTTATTACTGTCTCAGAGTTTATAGTACCCCTCGGACGTTTCGGCCCAAGGAC 305
DB 243 TTTTGGCACTTACTACTGTCTCAGAGTTCATCTCAGCAGTTCAGCTTCCCTAGCACTTTGGCCCTGGAC 302

QY 306 CAAGTGGAAATCAAA 321
DB 303 CAAGTGGATATCAAA 318

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 201
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-240-274-201

Query Match 81.5%; Score 261.6; DB 3; Length 321;
Best Local Similarity 89.2%; Pred. No. 2.4e-78;
Matches 282; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACATCAC 65
DB 3 CGAGTCAACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACATCAC 62

QY 66 TTGCGAGGCAAGTCAAGATAGTATTTAAATTTGGTATCAGCAGAAACCCAGGAA 125
DB 63 TTGCGGGCAAGTCAAGATAGTATTTAAATTTGGTATCAGCAGAAACCCAGGAA 122

QY 126 AGCTCTTAAGTCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTT 185
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QY 186 CAGCGGCAAGTCTGAGTCTGGGACAGAGTTCATCTCAGCTTCAGCAGCCTGAGCTCAAGA 245
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QY 306 CAAGTGGAAATCAAA 321
DB 303 CAAGTGGATATCAAA 318

RESULT 13
US-09-240-274-215
Sequence 215, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 215
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH46
US-09-240-274-215

Query Match 81.5%; Score 261.6; DB 3; Length 321;
Best Local Similarity 89.2%; Pred. No. 2.4e-78;
Matches 282; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACATCAC 65
DB 3 CGAGTCAACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACATCAC 62

QY 66 TTGCGAGGCAAGTCAAGATAGTATTTAAATTTGGTATCAGCAGAAACCCAGGAA 125
DB 63 TTGCGGGCAAGTCAAGATAGTATTTAAATTTGGTATCAGCAGAAACCCAGGAA 122


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RESULT 15
US-09-240-274-211
; Sequence 211, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-240-274-211

Query Match      81.0%; Score 260; DB 3; Length 321;
Best Local Similarity 88.9%; Pred. No. 8.3e-78;
Matches 281; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY      6 CCAGATGACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGGACAGAGTCACCATCAC 65
DB      3 CGAGCTCACTCAGTCTCCATCTCCCTGTCGATCTGTAGGAGACAGAGTCACCATCAC 62

QY     66 TTCAGGGCAAGTCAGACATTTAGGTATTTATTTATTTGTTATCAGCAGAAACCCAGAAA 125
DB     63 TTCCCGGGCAAGTCAGAGCATTTAGGTATTTATTTATTTGTTATCAGCAGAAACCCAGGAA 122

QY    126 AGCTCCTAAGCTCCTGATCTATCTGTCATCCAGTTTGCAGAGTGGGGTCCCATCAAGGTT 185
DB    123 ATCCCTAAGCTCCTGATCTATCTGTCATCCAGTTTGCAGAGTGGGGTCCCATCAAGGTT 182

QY    186 CAGCGGAGTGGATCTGGGACAGAGTTCACTCTCAGCGTCAGCAGCCTGACGCTGAGAA 245
DB    183 CAGTGCAGTGGATCTGGGACAGAGTTCACTCTCAGCATCAGCAGTCTGCAACCTGAGAA 242

QY    246 TTTTGGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTGGGCCAAGGGAC 305
DB    243 TTTTGCACCTTACTACTGTCTACAGTTTATAGTACCCCTCGGCTTTGGGCCCTGGGAC 302

QY    306 CAAGGTGGAATCAAA 321
DB    303 CAAAGTGGATATCAAA 318

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Search completed: June 19, 2004, 05:42:26
Job time : 65 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-019-441A-5_COPY_67_387

Perfect score: 321
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 2488216

Minimum DB seq length: 0
Maximum DB seq length: 321

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	269.6	84.0	321	10	US-09-848-798-221
5	269.6	84.0	321	10	US-09-848-798-222
6	268.2	83.6	321	15	US-10-172-317-3
7	268.2	83.6	321	15	US-10-320-094-3
8	268	83.5	321	10	US-09-848-798-105
9	266.6	83.1	321	15	US-09-851-614-1
10	266.6	83.1	321	15	US-10-035-637-1
11	266.4	83.0	321	10	US-09-848-798-107
12	266.4	83.0	321	10	US-09-848-798-216
13	265	82.5	321	15	US-10-060-585-9
14	264.8	82.5	321	10	US-09-848-798-98

15	264.8	82.5	321	10	US-09-848-798-104
16	264.8	82.5	321	10	US-09-848-798-207
17	263.4	82.1	321	15	US-10-073-644C-3
18	261.6	81.5	321	10	US-09-848-798-201
19	261.6	81.5	321	10	US-09-848-798-215
20	261.6	81.5	321	10	US-09-848-798-217
21	260.2	81.1	321	13	US-10-363-349-9
22	260.2	81.1	321	15	US-10-324-453-21
23	260	81.0	321	10	US-09-848-798-211
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29	257	80.1	321	17	US-10-325-698-12
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33	255.4	79.6	321	15	US-10-091-300-32
34	253.8	79.1	318	8	US-08-844-215-20
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39	253.6	79.0	321	10	US-09-848-798-213
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44	250.6	78.1	321	16	US-10-302-356A-36
45	250.6	78.1	321	16	US-10-163-657A-36

ALIGNMENTS

RESULT 1

US-10-663-244-78
; Sequence 78, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotide
US-10-663-244-78

Query Match 84.5%; Score 271.4; DB 17; Length 321;
Best Local Similarity 90.3%; Fred. No. 1.3e-80;
Matches 290; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY	1	GACATCCAGATGACCCAGTCTCCATCTTCCTCGTCTGTCATCTGTAGGGACAGATCAC	60
DB	1	GACATCCAGATGACCCAGTCTCCATCTTCCTCGTCTGTCATCTGTAGGGACAGATCAC	60
QY	61	ATCATTCTCAGGGCAGTACAGCAGATAGTATTATTTAAATTTGTTATCAGCAGAAACA	120
DB	61	ATCATTCTCAGGGCAGTACAGCAGATAGTATTATTTAAATTTGTTATCAGCAGAAACA	120

Qy	121	GGAAAGCTCC	TAAAGCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTCCCATCA	180
Db	121	GGAAAGCCCT	TAAAGCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTCCCATCA	180
Qy	181	AGSTTCAGCG	CAGTGGATCTGGGACAGATTCACTCTCAACGCTCAGACGCTGCAGCCT	240
Db	181	AGSTTCAGT	GGCAGTGGATCTGGGACAGATTCACTCTCAACATCAGCAGCTCTGCACCT	240
Qy	241	GAAGATTTTG	CGCACTTATTACTGCTCAGAGTTTATAGTACCCCTCGAGCTTCGGGCCAA	300
Db	241	GAAGATTTTG	CAACTTACTCTGTCACAGAGTTACTCTACCCCTCGACTTTCGGCCCT	300
Qy	301	GGGACCAAG	GGTGCAAATCAAA	321
Db	301	GGGACCAAG	TGGATCAAA	321

RESULT 2

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US-09-848-798-102
; Sequence 102, Application US/09848798
; Publication No. US20030040605A1
GENERAL INFORMATION:
; APPLICANT: Siegel, Donald E.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09S96-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-102

```

RESULT 3

```

US-09-848-798-218
; Sequence 218, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-08-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-218

Query Match      84.0%; Score 269.6; DB 10; Length 321;
Best Local Similarity 90.8%; Pred.No. 5.1e-80;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0

QY      6 CCAGATGACCCAGTCTCCATCTTCCTCTCTGCAATCTGTAGGGACAGAGTCACCATCAC 65
DB      3 CGAGCTACCCAGTCTCCATCTTCCTCTCTGCAATCTGTAGGAGACAGAGTCACCGTCAC 62

QY      66 TTGCGAGGCACTGAGGACATAGTATTATTAAATTTGGTATCAGCAGAAACCAGGAA 124
DB      63 TTGCGGAGGCACTGAGGACATAGCAGCTATTAAATTTGGTATCAGCAGAAACCAGGAA 124

QY      126 AGCTCCTAAGCTCCATGATCTATGTTGCAATCCAGTTTGCAAGTGGGTCCCATCAAGTT 181
DB      123 AGCCCTAAGCTCCATGATCTATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGTT 183

QY      186 CAGCGGCACTGATCTGGGACAGAGTTTCACCTCACCGTCAGCAGCTGCGAGCTGAAGA 242
DB      183 CAGTGGCACTGATCTGGGACAGATTTCACTCTCACCATCAGCACTCTGCACCTGAGA 242

QY      246 TTTTCGCACTTATTACTGCTACAGTTTATAGTACCCCTCGGAGCTTCGCGCCAAAGGAC 308
DB      243 TTTTGCACCTTACTACTGCTCAACAGATTACAGTACCCCGTGGAGCTTCGCGCCAAAGGAC 308

QY      306 CAAAGTGGAAATCAA 321
DB      303 CAAAGTGGAAATCAA 318

RESULT 4
US-09-848-798-221
; Sequence 221, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 321
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-221

Query Match      84.0%; Score 269.6; DB 10; Length 321;
Best Local Similarity 90.8%; Pred. No. 5.1e-80;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTCCCTGTCGTCATCTGTAGGGGACAGAGTCACCATCAC 65
DB 3 CGAGCTCACCCAGTCTCCATCTCCCTGTCGTCATCTGTAGGGGACAGAGTCACCATCAC 62
QY 66 TTGCGGGCAAGTCAGGACATTAGTATTATTTAAATTTGGTATCAGAGAAACCGAGGAA 125
DB 63 TTGCGGGCAAGTCAGGACATTAGTATTATTTAAATTTGGTATCAGAGAAACCGAGGAA 122
QY 126 AGCTCTAAGCTCCGATCTATGTTTGCATCCAGTTTGCAAGTGGGTCCTCCATCAAGGTT 185
DB 123 AGCCCTAAGCTCCGATCTATGTTTGCATCCAGTTTGCAAGTGGGTCCTCCATCAAGGTT 182
QY 186 CAGCGGAGTGGATCTGGGACAGATTCACTCTCACGCTCAGCAGCCTGCAGCCTGGAAGA 245
DB 183 CAGTGGCAGTGGATCTGGGACAGATTCACTCTCACGCTCAGCAGCCTGCAGCCTGGAAGA 242
QY 246 TTTTCGGACTTATTACTCTACAGGTTTATAGTACCCCTCGGAGGTTTCGGCCAGGGAC 305
DB 243 TTTTCGAACTTACTACTGTCAACAGATTACAGTACCCCTCGGAGGTTTCGGCCAGGGAC 302
QY 306 CAAGTGGAAATCAAA 321
DB 303 CAAGTGGAAATCAAA 318

RESULT 5
US-09-848-798-222
; Sequence 222, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-222

Query Match      84.0%; Score 269.6; DB 10; Length 321;
Best Local Similarity 90.8%; Pred. No. 5.1e-80;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTCCCTGTCGTCATCTGTAGGGGACAGAGTCACCATCAC 65
DB 3 CGAGCTCACCCAGTCTCCATCTCCCTGTCGTCATCTGTAGGGGACAGAGTCACCATCAC 62
QY 66 TTGCGGGCAAGTCAGGACATTAGTATTATTTAAATTTGGTATCAGAGAAACCGAGGAA 125
DB 63 TTGCGGGCAAGTCAGGACATTAGTATTATTTAAATTTGGTATCAGAGAAACCGAGGAA 122
QY 126 AGCTCTAAGCTCCGATCTATGTTTGCATCCAGTTTGCAAGTGGGTCCTCCATCAAGGTT 185
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DB 123 AGCCCTAAGCTCTCTGATCTATGTCATCCAGTTTCCAAAGTGGGTCCTCCATCAAGTT 182
QY 186 CAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACGCTCAGCAGCCTGCAGCCTGGAAGA 245
DB 183 CAGTGGCAGTGGATCTGGGACAGATTCACTCTCACGCTCAGCAGCCTGCAGCCTGGAAGA 242
QY 246 TTTTCGGACTTATTACTCTCTACAGGTTTATAGTACCCCTCGGAGGTTTCGGCCAGGGAC 305
DB 243 TTTTCGAACTTACTACTGTCAACAGATTACAGTACCCCTCGGAGGTTTCGGCCAGGGAC 302
QY 306 CAAGTGGAAATCAAA 321
DB 303 CAAGTGGAAATCAAA 318

RESULT 6
US-10-172-317-3
; Sequence 3, Application US/10172317
; Publication No. US20030091561A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus A.
; APPLICANT: Halk, Edward
; APPLICANT: Gerritsen, Arnout F.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
; TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR (EGFR)
; FILE REFERENCE: GMI-020
; CURRENT APPLICATION NUMBER: US/10/172,317
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/298,172
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-172-317-3

Query Match      83.6%; Score 268.2; DB 15; Length 321;
Best Local Similarity 89.7%; Pred. No. 1.5e-79;
Matches 288; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCGTCATCTGTAGGGGACAGAGTCACC 60
DB 1 GCCATCCAGTGTACCCAGTCTCCATCTCCCTGTCGTCATCTGTAGGGGACAGAGTCACC 60
QY 61 ATCACTTGCAGGCGCAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 120
DB 61 ATCACTTGCAGGCGCAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 120
QY 121 GGAAGAGCTCCTAAGCTCCTGATCTATGTTGCAATCCAGTTTGCAAGTGGGTCCTCATCA 180
DB 121 GGAAGAGCTCCTAAGCTCCTGATCTATGATGCTCCAGTTTGGAAAGTGGGTCCTCATCA 180
QY 181 AGTTTCAGCGGCGAGTGTGAGGACAGAGTTCACCTCTCACGCTCAGCAGCCTGCAGCCT 240
DB 181 AGTTTCAGCGGCGAGTGTGAGGACAGAGTTCACCTCTCACGCTCAGCAGCCTGCAGCCT 240
QY 241 GAAGATTTTCGCGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGAGGTTTCGGCAA 300
DB 241 GAAGATTTTCGCGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGAGGTTTCGGCAA 300
QY 301 GGGACCAAGTGGAAATCAAA 321
DB 301 GGGACCAAGTGGAGATCAAA 321

RESULT 7
US-10-320-094-3
; Sequence 3, Application US/10320094
; Publication No. US20030194403A1
; GENERAL INFORMATION:
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; APPLICANT: van de Winkel, Jan G.J.  
; APPLICANT: van Dijk, Marcus A.  
; APPLICANT: Halk, Edward  
; APPLICANT: Gerritsen, Arnout F.  
; APPLICANT: Petersen, Jorgen  
; APPLICANT: Baadsgaard, Ole  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO  
; FILE REFERENCE: GM-020CF  
; CURRENT APPLICATION NUMBER: US/10/320,094  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: US 60/298172  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: OS 10/172317  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-320-094-3
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Query Match 83.6%; Score 268.2; DB 15; Length 321;
Best Local Similarity 89.7%; Pred. No. 1.5e-79;
Matches 288; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 GACATCCAGATGACCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGACAGAGTCAC 60
DB 1 GCCATCCAGTTGACCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGACAGAGTCAC 60

QY 61 ATCACTTGCGGGCAGTGCAGACATTAGGTATTATTTAAATTTGGTATCATCAGCAAACCA 120
DB 61 ATCACTTGCGGGCAGTGCAGACATTAGGTATTATTTAAATTTGGTATCATCAGCAAACCA 120

QY 121 GGAAAAGCTCTTAAGCTCTGAATCTGATCTGCATCCAGTTTGCATAAGTGGGGTCCCATCA 180
DB 121 GGAAAAGCTCTTAAGCTCTGAATCTGATCTGCATCCAGTTTGCATAAGTGGGGTCCCATCA 180

QY 181 AGTTTCAGCGGAGTGGATCTGGGACAGATTTCACTCTCACATCAGCAGCTGCAGCCT 240
DB 181 AGTTTCAGCGGAGTGGATCTGGGACAGATTTCACTCTCACATCAGCAGCTGCAGCCT 240

QY 241 GAAGAATTTTGGCACTTATTACTGTCTVACAGSTTTATAGTACCCCTGGAGCTTCGGCAA 300
DB 241 GAAGAATTTTGGCACTTATTACTGTCTVACAGSTTTATAGTACCCCTGGAGCTTCGGCAA 300

QY 301 GGGACCAAGGTGGAAATCAA 321
DB 301 GGGACCAAGGTGGAGATCAA 321

RESULT 8
US-09-848-798-105
Sequence 105, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: SORTING METHOD FOR PRODUCTION THEREOF
CURRENT APPLICATION NUMBER: US/09/848,798
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 105
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: anti-Rh(D) chain I05
US-09-848-798-105

Query Match 83.5%; Score 268; DB 10; Length 321;
Best Local Similarity 90.5%; Pred. No. 1.8e-79;
Matches 286; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGACAGAGTCACCATCAC 65
DB 3 CGAGCTCACCCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGACAGAGTCACCATCAC 62

QY 66 TTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCATCAGCAAACCAAGGAAA 125
DB 63 TTGCAGGGCAAGTCAGGACATTAGGAGGTATTATTTAAATTTGGTATCATCAGCAAACCAAGGAAA 122

QY 126 AGCTCTTAAGCTCTCTGATCTATGTTGATCCAGTTTGCATAAGTGGGGTCCCATCAGGTT 185
DB 123 AGCCCCTAAGCTCTCTGATCTTTGCTGATCCAGTTTGCATAAGTGGGGTCCCATCAGGTT 182

QY 186 CAGCGGCGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTTCGAGCCTGAAGA 245
DB 183 CACTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTTCGCAACCTGAAGA 242

QY 246 TTTTCGCACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTTCGGCCHAGGGAC 305
DB 243 TTTTCGCACTTACTACTGTCAACAGAGTTACAGTACCCCTCAAAAGTTTCGGCCAAGGGAC 302

QY 306 CAAGGTGGAATCAA 321
DB 303 CAAGGTGGAATCAA 318

RESULT 9
US-09-851-614-1
Sequence 1, Application US/09851614
Publication No. US20030167502A1
GENERAL INFORMATION:
APPLICANT: Deco, Yashwant M.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
FILE REFERENCE: MXI-166
CURRENT APPLICATION NUMBER: US/09/851,614
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: USSN 60/203,126
PRIOR FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: USSN 60/230,739
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(321)
US-09-851-614-1

Query Match 83.1%; Score 266.6; DB 10; Length 321;
Best Local Similarity 89.4%; Pred. No. 5.2e-79;
Matches 287; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GCATCCAGATGACCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGACAGAGTCAC 60
DB 1 GCATCCAGATGACCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGACAGAGTCAC 60

QY 61 ATCACTTGCGGGCAGTGCAGACATTAGGTATTATTTAAATTTGGTATCATCAGCAAACCA 120
DB 61 ATCACTTGCGGGCAGTGCAGACATTAGGTATTAGAGTGGTGTAGCTGTGATCATCAGCAAACCA 120

QY 121 GGAAAAGCTCTTAAGCTCTGAATCTGATCTGCATCCAGTTTGCATAAGTGGGGTCCCATCA 180

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Db 121 GAGAAAGCCCTAAGTCCCTGATCTATGTCGATCCAGTTTGCAGAGTGGGTCCTCCATCA 180
Qy 181 AGGTTTCAGGCGCAGTGGATCTGGACAGAGTTTCACTCTCACCCTGACAGCCTTGCAGCCT 240
Db 181 AGGTTTCAGGCGCAGTGGATCTGGACAGAGTTTCACTCTCACCCTGACAGCCTTGCAGCCT 240
Qy 241 GAAGATTTTGGCACTTATCTGTCACAGTTTATAGTACCCCTCGAGGTTGGGCCAA 300
Db 241 GAAGATTTTGGCACTTATCTGTCACAGTTTATAGTACCCCTCGAGGTTGGGCCAA 300
Qy 301 GGGACCAAGGTGGAATCAA 321
Db 301 GGGACCAAGGTGGAATCAA 321

RESULT 10
US-10-035-637-1
; Sequence 1, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keller, Tidor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035,637
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/851,614
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USSN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(321)
US-10-035-637-1
Query Match 83.1%; Score 266.6; DB 15; Length 321;
Best Local Similarity 89.4%; Pred. No. 5.2e-79;
Matches 287; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGATCTGTAGGGAGAGAGTCAACC 60
Db 1 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGATCTGTAGGGAGAGAGTCAACC 60
Qy 61 ATCATTGCGGGCGAGTCAAGGATTTAGGAGTGGTATGATGATGATGATGATGATGATGATGAT 120
Db 61 ATCATTGCGGGCGAGTCAAGGATTTAGGAGTGGTATGATGATGATGATGATGATGATGATGAT 120
Qy 121 GGAAGAGTCTTAAAGTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Db 121 GGAAGAGTCTTAAAGTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Qy 181 AGGTTTCAGGCGCAGTGGATCTGGACAGAGTTTCACTCTCACCCTGACAGCCTTGCAGCCT 240
Db 181 AGGTTTCAGGCGCAGTGGATCTGGACAGAGTTTCACTCTCACCCTGACAGCCTTGCAGCCT 240
Qy 241 GAAGATTTTGGCACTTATCTGTCACAGTTTATAGTACCCCTCGAGGTTGGGCCAA 300
Db 241 GAAGATTTTGGCACTTATCTGTCACAGTTTATAGTACCCCTCGAGGTTGGGCCAA 300
Qy 301 GGGACCAAGGTGGAATCAA 321
Db 301 GGGACCAAGGTGGAATCAA 321
```

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RESULT 11
US-09-848-798-107
; Sequence 107, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 107
US-09-848-798-107
Query Match 83.0%; Score 266.4; DB 10; Length 321;
Best Local Similarity 90.2%; Pred. No. 6.1e-79;
Matches 285; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 6 CGAGATGACCCAGTCTCCATCTTCCCTGCTGCTGATCTGTAGGGAGAGAGTCAACCAC 65
Db 3 CGAGTCAACCCAGTCTCCATCTTCCCTGCTGCTGATCTGTAGGGAGAGAGTCAACCAC 62
Qy 66 TTGCGGGCAAGTCAAGCAGATTTAGGATTTATTTAAATTTGGTATTCAGCAGAAACAGGAA 125
Db 63 TTGCGGGCAAGTCAAGCAGATTTAGGATTTATTTAAATTTGGTATTCAGCAGAAACAGGAA 122
Qy 126 AGCTCTTAAGTCTCTGATCTATGTTGATCCAGTTTGCAGAGTGGGTCCCATCAGGTT 185
Db 123 AGCCCTTAAGTCTCTGATCTATGTTGATCCAGTTTGCAGAGTGGGTCCCATCAGGTT 182
Qy 186 CAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCCTGACAGCCTGAGCCTGAAGA 245
Db 183 CAGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCCTGACAGCCTGAGCCTGAAGA 242
Qy 246 TTTTGGCACTTATTTACTGCTCTACAGGTTTATAGTACCCCTCGAGCCTTGGCCAGGGAC 305
Db 243 TTTTGGCACTTATTTACTGCTCTACAGGTTTATAGTACCCCTCGAGCCTTGGCCAGGGAC 302
Qy 306 CAGGTGGAATCAA 321
Db 303 CAGGTGGAATCAA 318

RESULT 12
US-09-848-798-216
; Sequence 216, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
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Search completed: June 19, 2004, 06:26:45
Job time : 286 secs

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OM nucleic - nucleic search, using sw model

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Title: US-09-019-441a-5_COPY_67_387
Perfect score: 321
Sequence: 1 gacatccagatgaccagtc.....gsaccaagtggaaatcaaa 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 9921772

Minimum DB seq length: 0
Maximum DB seq length: 321

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

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- 2: em_esthum:*
- 3: em_estlin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_estl:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_psg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	223.6	69.7	269	10 AW404590	AW404590 UI-HF-BL0
2	216.8	67.5	284	10 BF869849	BF869849 IL3-ET011
3	213.4	66.5	270	10 AW406247	AW406247 UI-HF-BL0
4	209.4	65.2	315	10 AW406545	AW406545 UI-HF-BL0

5	204.8	63.8	254	10 AW406058	AW406058 UI-HF-BL0
6	203.8	63.5	303	9 AA300891	AA300891 EST14031
7	203.6	63.4	303	9 AA300788	AA300788 EST13648
8	200	62.3	276	10 BF095147	BF095147 PM3-UT005
9	198.8	61.9	280	10 AW407313	AW407313 UI-HF-BL0
10	197.2	61.4	304	10 BF869187	BF869187 IL3-ET011
11	195.6	60.9	301	9 AA377295	AA377295 EST9837
12	192.6	60.0	283	10 AW404303	AW404303 UI-HF-BL0
13	190.4	59.3	321	12 BM856175	BM856175 K-EST0139
14	190.2	59.3	276	14 CD686963	CD686963 EST1484 h
15	189.8	59.1	252	10 AW407923	AW407923 UI-HF-BL0
16	188.4	58.7	282	9 AA300491	AA300491 EST13404
17	187.8	58.5	257	10 BE720151	BE720151 RC3-HT088
18	184.4	57.4	248	10 AW404355	AW404355 UI-HF-BL0
19	184	57.3	279	10 BE163116	BE163116 QV3-HT045
20	182.2	56.8	271	10 BF870341	BF870341 IL3-ET011
21	182	56.7	312	12 BM825516	BM825516 K-EST0097
22	181.6	56.6	292	9 AA295508	AA295508 EST100751
23	180.4	56.2	297	10 BF869666	BF869666 IL3-ET011
24	179.6	56.0	318	14 CD709351	CD709351 EST25878
25	177.8	55.4	289	10 AW860832	AW860832 OV0-CT038
26	177.8	55.4	297	9 AA301343	AA301343 EST14275
27	176.2	54.9	229	10 BF870338	BF870338 IL3-ET011
28	176.2	54.9	243	10 AW404283	AW404283 UI-HF-BL0
29	175.8	54.8	292	10 AW951839	AW951839 EST363909
30	174.6	54.4	275	14 CD690814	CD690814 EST7337 h
31	172.2	53.6	218	12 BM769908	BM769908 K-EST0053
32	171.6	53.5	286	9 AA327542	AA327542 EST30974
33	170.4	53.1	287	14 CD708479	CD708479 EST25006
34	169.8	52.9	315	10 AW405131	AW405131 UI-HF-BL0
35	169.2	52.7	306	10 BF868804	BF868804 IL3-ET011
36	167.8	52.3	295	10 AW366663	AW366663 RC3-HT014
37	166.2	51.8	289	9 AA295841	AA295841 EST101050
38	165	51.4	317	10 AW404261	AW404261 UI-HF-BL0
39	164.2	51.2	280	10 AW800017	AW800017 PM4-UM005
40	164.2	51.2	288	9 AA368827	AA368827 EST77840
41	163.8	51.0	320	14 CD706092	CD706092 EST22619
42	162.6	50.7	321	14 CD693795	CD693795 EST10318
43	162	50.5	320	12 BM823161	BM823161 K-EST0094
44	161.6	50.3	288	14 T27581	T27581 EST100107 H
45	161	50.2	301	10 AW407044	AW407044 UI-HF-BL0

ALIGNMENTS

RESULT 1
AW404590
LOCUS UI-HF-BL0-acb-d-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3058588 5', mRNA sequence.
ACCESSION AW404590
VERSION AW404590.1 GI:6923647
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 269)
NIH-National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS Unpublished (1999)
TITLE Contact: Robert Strausberg, Ph.D.
JOURNAL Email: cgapbs-remail.nih.gov
COMMENT Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.B. Consortium/LLNL at: www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source
1. .269
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3058588"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC 37"
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 69.7%; Score 223.6; DB 10; Length 269;
Best Local Similarity 90.8%; Pred. No. 2.1e-62;
Matches 238; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 36 TGCATCTGTAGGACAGAGTCACCATCATTGCGAGGCAAGTCAGGACATTAGGTATTA 95
Db 8 TGCATCTGTAGGACAGAGTCACCATCATTGCGAGGCAAGTCAGGACATTAGGACGCTA 67
QY 96 TTTAAATGTGTATCAGCAGAAACAGGAAAGCTCTAAGCTCTCTATCTATGTGATC 155
Db 68 TTTAAATGTGTATCAGCAGAAACAGGAAAGCTCTAAGCTCTCTATCTATGTGATC 127
QY 156 CAGTTTGCAAGTGGGGTCCCATCAAGTTTCAGGGGAGTGGATCTGGGACAGAGTTTCA 215
Db 128 CAATTTCGAAAGTGGGGTCCCATCAAGTTTCAGGGGAGTGGATCTGGGACAGAGTTTCA 187
QY 216 TCTCACCCTCAGAGCTGCGAGCTGAAGTTTGGGACATTATTTACTGTCTACAGGTTTA 275
Db 188 TCTCACCCTCAGAGCTGCGAGCTGAAGTTTGGGACATTATTTACTGTCTACAGAGGTTA 247
QY 276 TAGTACCCCTCGAGCTTGGGC 297
Db 248 CAGTACCCCTCGAGCTTGGGC 269

RESULT 2
BF69849
LOCUS
IL3-ET0114-251000-317-007 ET0114 Homo sapiens cDNA, mRNA sequence.
DEFINITION
BF69849
VERSION
BF69849.1 GI:12259979
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 284)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zagó,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&t2=IL3-ET0114-
251000-317-007&t3=2000-10-25&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 185.
Location/Qualifiers
1. .284
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0114"
/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSITES PCR (U.S. Letters Patent application
No. 196.716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 67.5%; Score 216.8; DB 10; Length 284;
Best Local Similarity 85.2%; Pred. No. 3.7e-60;
Matches 242; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 37 GCATCTGTAGGACAGAGTCACCATCATTGCGAGGCAAGTCAGGACATTAGGTATTA 96
Db 1 GCATCTGTAGGACAGAGTCACCATCATTGCGAGGCAAGTCAGGACATTAGGAAATGAT 60
QY 97 TTAATTTGTGTATCAGCAGAAACAGGAAAGCTCTAAGCTCTCTATCTATGTGATCC 156
Db 61 TTAGGCTGTGTATCAGCAGAAACAGGAAAGCTCTAAGCTCTCTATCTATGTGATCC 120
QY 157 AGTTTGCAAAGTGGGGTCCCATCAAGTTTCAGGGGAGTGGATCTGGGACAGAGTTCACT 216
Db 121 AGTTTGCAAAGTGGGGTCCCATCAAGTTTCAGGGGAGTGGATCTGGGACAGAGTTCACT 180
QY 217 CTCACCGTCAGAGCTGCGAGCTGAAGTTTGGGACATTATTTACTGTCTACAGGTTTAT 276
Db 181 CTTCATCATCAGAGCTGCGAGCTGAAGTTTGGGACATTATTTACTGTCTACAGGTTTAT 240
QY 277 AGTACCCCTCGAGAGCTTGGGCAAGGACCAAGTGGGAAATCAA 320
Db 241 AGTTACCCCTCGAGAGCTTGGGCAAGGACCAAGTGGGAAATCAA 284

RESULT 3
AW406247
LOCUS
UI-HF-BL0-acp-e-11-0-UI.r1 NIH_MGC 37 Homo sapiens cDNA clone
DEFINITION
IMAGE:3059828 5', mRNA sequence.
ACCESSION
AW406247
VERSION
AW406247.1 GI:6925304
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 270)
NIH_MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers

FEATURES

source

1. 270
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3059828"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/note="Vector: p7773-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 66.5%; Score 213.4; DB 10; Length 270;
Best Local Similarity 88.2%; Pred. No. 4.7e-59; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 31;

QY 7 CAGATGACCCAGTCTCCATCTTCCCTGCTGCACTGTAGGGGACAGAGTCAACCATCACT 66
Db 8 CAGATGACCCAGTCTCCATCTTCCCTGCTGCACTGTAGGGGACAGAGTCAACCATCACT 67

QY 67 TCGAGGGCAAGTCAGGACATTAGGTATTTAAATTTGGTATCAGGAAACCGAGAAA 126
Db 68 TCGCATGCGAGTCAGGACATTACCAACTATTTACATTTGGTATCATCAGAAACCGAGAAA 127

QY 127 GCTCTTAGCTCCTGATCTGTGTCATCTGCTCCAGTTTGGCAAGTGGGTCCTCAAGGTTTC 186
Db 128 GCCCTTAGCTCCTGATCTAGTGCATCCAAATTTGGAAACAGGGTCCCATCAAGTTTC 187

QY 187 AGCGGCACTGGATCGGACAGAGTCACTCTCCCGTCAGAGCGCTGCAGCCTGAAGAT 246
Db 188 AGTGGAGTGGATCGGACAGAGATTTACTTTCACCATCAGTAGCCTGCAGCCTGAAGAT 247

QY 247 TTGCGACTTATTACTGCTACA 269
Db 248 ATTGCAACATATTACTGCAACA 270

RESULT 4
AW406545
LOCUS
DEFINITION
UI-HF-BL0-ach-e-04-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3060199 5', mRNA sequence.
ACCESSION
AW406545
VERSION
AW406545.1 GI:6925602
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 315)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers

FEATURES

source

1. 315
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3060199"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/note="Vector: p7773-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 65.2%; Score 209.4; DB 10; Length 315;
Best Local Similarity 89.6%; Pred. No. 1.1e-57; Indels 0; Gaps 0;
Matches 225; Conservative 0; Mismatches 26;

QY 1 GATATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCACTGTAGGGGACAGAGTCAAC 60
Db 65 GATATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCACTGTAGGGGACAGAGTCAAC 124

QY 61 ATCACTTTCAGGGCAAGTCAGGACATTAGGTATTTAAATTTGGTATCAGGAAACCA 120
Db 125 ATTACTTTCGGGCAAGTCAGTATATTAGTACTATTTAAATTTGGTATCAGGAAACCA 184

QY 121 GGAAGACTCTTAAGCTCCTGATCTGTCATCTGTCAGATTTGCAAGTGGGTCCTCATCA 180
Db 185 GGGAGAGCCCTCAGGCTCCTGATCTATCTGCTTCCAGTTTGCAGATTTGCAAGTGGGTCCTCATCA 244

QY 181 AGGTTTCAGCGGCGAGTGGATCTGGGACAGAGTTCACCTCTCAACGTCAGAGCCTGCAGCCT 240
Db 245 AGGTTTCAGTGGCAGTGGATCTGGGACAGAGTTCACCTCTCAACGTCAGAGCCTGCAGCCT 304

QY 241 GAAGATTTTGC 251
Db 305 GAAGATTTTGC 315

RESULT 5
AW406058
LOCUS
DEFINITION
UI-HF-BL0-ach-e-01-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059040 5', mRNA sequence.
ACCESSION
AW406058
VERSION
AW406058.1 GI:6925150
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 254)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers

1. 254
/organism="Homo sapiens"
/mol_type="mRNA"

TITLE Initial assessment of human gene diversity and expression patterns
JOURNAL based upon 83 million nucleotides of cDNA sequence
MEDLINE Nature 377 (6547 Suppl), 3-174 (1995)
PUBMED 96026280
COMMENT 7566098
 Other ESTs: THC167177
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@igr.org

For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.
FEATURES
 source
 1..303
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="ATCC (inhost):192224"
 /db_xref="taxon:9606"
 /sex="male"
 /dev_stage="adult"
 /clone_lib="Testis tumor"
 /note="Organ: testis; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI"

ORIGIN
 Query Match 63.4%; Score 203.6; DB 9; Length 303;
 Best Local Similarity 91.5%; Pred. No. 8.5e-56;
 Matches 215; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 2 ACATCCAGATGACCCAGTCCATCTCCCTGTCGATCTGTAGGGACAGATCACA 61
 DB 69 ACATCCAGATGACCCAGTCCATCTCCCTGTCGATCTGTAGGGACAGATCACA 128
 QY 62 TCACCTGTCAGGCGACAGTCCAGTATAGTATATTTAAATTGGTATCAGCAGAAACAC 121
 DB 129 TCACCTGTCAGGCGACAGTCCAGTATAGTATATTTAAATTGGTATCAGCAGAAACAC 188
 QY 122 GAAAGCTCCTAAGCTCTGATCTATGTGATCAGTTTGCAGTTGGAAAGTGGTCCCATCA 181
 DB 189 GGAAGAGCCCTAATCTCCTGATCTCTGCTGCATCCAGTTTGCAGTTGGAAAGTGGTCCCATCA 248
 QY 182 GGTTCAGGCGAGTGTGATCTGGACAGAGTTCACTCTCAGCTCAGCAGCTGCA 236
 DB 249 GGTTCAGTGTGATGTGGAGAGATTTCATCTCAGCAGTCTGCA 303

RESULT 8
BF095147 276 bp mRNA linear EST 19-OCT-2000
LOCUS PM3-UT0058-060900-004-e03 UT0058 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF095147
ACCESSION BF095147.1 GI:10900766
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 276)
AUTHORS Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
TITLE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL 20202663
MEDLINE

PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPSP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=PM3-UT0058-060>)
 900-004-e03kt3=2000-09-06&t4=1
 Seq primer: puc 18 forward
 High quality sequence start: 15
 High quality sequence stop: 276.
FEATURES
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="UT0058"
 /note="Organ: uterus tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN
 Query Match 62.3%; Score 200; DB 10; Length 276;
 Best Local Similarity 91.4%; Pred. No. 1.2e-54;
 Matches 234; Conservative 0; Mismatches 20; Indels 2; Gaps 2;
 QY 15 CCATCTCCATCTTCCCTGTCGATCTGTAGGGACAGATCACCATCACTTCAGGGC 74
 DB 22 CCAGTCTCCATCTTCCCTGTCG-ATCTGTAGGACAGAGTCCATACTTCCCGGC 80
 QY 75 AAGTCAGACATTAGGTATTATTAAATTGGTATCAGCAGAAACAGGAAAGCTCTAA 134
 DB 81 AAGTCAGACATTAGCAGCTATTAAATTGGTATCAGCAGAAACAGG-AAAGCCCCATA 139
 QY 135 GCTCCTGATCTATGTCATCCAGTTTGCAGAGTGGGTCCTCATCAAGTTTCAGCGCAG 194
 DB 140 GCTCCTGATCTATGTCATCCAGTTTGCAGAGTGGGTCCTCATCAAGTTTCAGTGGCAG 199
 QY 195 TGGATCTGGGACAGATTCATCTCAGCTCAGCAGCTGCGAGCTTGAAGATTTTGGAC 254
 DB 200 TGGATCTGGGACAGATTCATCTCAGCTCAGCAGCTGCGAGCTTGAAGATTTTGGAC 259
 QY 255 TTATTACTGTCTACAG 270
 DB 260 TTACTACTGTACACAG 275

RESULT 9
AM407313 280 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BL0-adj-d-12-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3061702 5', mRNA sequence.
ACCESSION AM407313
VERSION AM407313.1 GI:6926370
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 280)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cga@pe-rmail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward

FEATURES

source
 1. .280
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3061702"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B LTI"
 /clone_lib="NIH MGC 37"
 /note="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaligo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 61.9%; Score 198.8; DB 10; Length 280;
 Best Local Similarity 85.7%; Pred. No. 3.1e-54;
 Matches 221; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
 QY 1 GACATCAGATGACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGACAGAGTCAAC 60
 DB 23 GACATCAGATGACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGACAGAGTCAAC 82
 QY 61 ATCACTTGCAGGGCAAGTCAGACATAGGTATTTAAATTTGGTATCAGCGAAACCA 120
 DB 83 ATCACTTGCAGGGCAAGTCAGATGATTTAGTGTGGCTGTGTCGAGAAACCA 142
 QY 121 GGAAGAGCTCTAAGCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCA 180
 DB 143 GGGAAAGCCCTAAGCTCTGATCTATAAGGCATCTAGTTTGAAGATAAGTTCCATCA 202
 QY 181 AGGTTTCAGCGCAGTGCATCTGGACAGATTCATCTCACCCTCAGCAGCCTGCAGCCT 240
 DB 203 AGGTTTCAGCGCAGTGCATCTGGACAGATTCATCTCACCCTCAGCAGCCTGCAGCCT 262
 QY 241 GAAGATTTCGACTTAT 258
 DB 263 GATGATTTCGACTTAT 280

RESULT 10

BF869187
 LOCUS 304 bp mRNA linear EST 17-JAN-2001
 DEFINITION IL3-ET0115-181000-294-F05 ET0115 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF869187
 VERSION BF869187.1 GI:12259317
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 304)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., Góes, P.S., Sucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

TITLE

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 {http://www.ludwig.org.br/scripts/gethtml2.pl?i=IL3&t2=IL3-ET0115-
 181000-294-F05&t3=2000-10-18&t4=1}

Seq primer: puc 18 forward

High quality sequence stop: 303.

FEATURES

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="ET0115"
 /note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 61.4%; Score 197.2; DB 10; Length 304;
 Best Local Similarity 82.5%; Pred. No. 1.1e-53;
 Matches 236; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 6 CCAGATGACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGACAGAGTCAACATCAC 65
 DB 1 CCAGATGACCCAGTCTTCCTCCACCTGTCGCTGTGTAGGACAGAGTCAACATCAC 60
 QY 66 TTGCGAGGCAAGTCAGGACATTAGGTATTTAAATTTGGTATCAGCGAAACCAAGGAAA 125
 DB 61 TTGCGGCGCAGTCAGACATTTAATAGTTGGTGGCTGGTATCAGCGAAACCAAGGAG 120
 QY 126 AGCTCTAGCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGCTCCCATCAAGGTT 185
 DB 121 AGCCCTAACTCTTAUCTACAGGCGGTCTACTTTAGAGAGTGGGTTCCCATCAAGGTT 180
 QY 186 CAGCGCAGTGGATCTGGGACAGAGTTCATCTCACCCTCAGCAGCCTGCAGCCTGAAGA 245
 DB 181 CAGCGCAGTGGATCTGGAAACAGAAATTCATCTCACCATCAGCAGCCTGCAGCCTGATGA 240
 QY 246 TTTTGGACTTATTACTGTCTACAGTTTATAGT 279
 DB 241 TTTCGCACTTATTCTTCGCAACAGATCATATT 274

RESULT 11

AA377295
 LOCUS 301 bp mRNA linear EST 21-APR-1997
 DEFINITION Small intestine II Homo sapiens cDNA 5' end similar to
 immunoglobulin kappa light chain, V region, mRNA sequence.
 ACCESSION AA377295
 VERSION AA377295.1 GI:2029613
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 301)
 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 53 row: D column: 11

High quality sequence stop: 321.

Location/Qualifiers

1. 321

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S14K402-53-D11"

/cell_line="K402"

/lab_host="Top10F"

/clone_lib="S14K402"

/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then dephosphorylated with tabacco acid pyrophosphatase (TAP). The dephosphorylated intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 59.3%; Score 190.4; DB 12; Length 321;
Best Local Similarity 88.8%; Pred. No. 2e-51;
Matches 206; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GACATCCAGATGACCCAGTCCATCTTCCCTCTGCTGCTAGTGGGACAGAGTCACC 60
DB 90 GACATCCAGATGACCCAGTCCATCTTCCCTCTGCTGCTAGTGGGACAGAGTCACC 149
QY 61 ATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTATTAATTGGTATCAGCAAAACCA 120
DB 150 ATCGTTGCCGGCAAGTCAGGACATTAGGTATTATTATTAATTGGTATCAGCAAAACCA 209
QY 121 GGAAGACTCTTAAGTCTTCGATCTATGTCATCCAGTTGCAAGTGGGTCACCATCA 180
DB 210 GGGAGAGCCCTAAGTCTTCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCA 269
QY 181 AGGTTTCAGGGCAGTGGATCTGGGACAGATTCACCTCTACCGTCAGCAGCC 232
DB 270 ATGTTTCAGTGGCAGTGGATCTGGGACAGATTCACCTCTACCGTCAGCAGTC 321

RESULT 14

CD686963
LOCUS
DEFINITION
EST3494 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION
CD686963
VERSION
CD686963.1 GI:32204374
KEYWORDS
EST.
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 276)

AUTHORS

Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.

Transcriptional Gene Expression Profile of Human Nasopharynx

Unpublished (2003)

Contact: Yixin Zeng

Cancer Center

Sun Yat-sen University

651 Dongfeng Road East, Guangzhou 510060, China

Tel: 86-1380-9770-743

Fax: 86-20-8775-4506

Email: yxzeng@gzsums.edu.cn.

Location/Qualifiers

1. 276

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue="nasopharynx"

/clone_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

Library from southern Chinese"

Library from southern Chinese"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3061236"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (lri)"
/clone_lib="NIH_MGC37"
/notes="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

```

ORIGIN

```

Query Match      59.1%; Score 189.8; DB 10; Length 252;
Best Local Similarity 92.2%; Pred. No. 2.7e-51;
Matches 200; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GACATCCAGATCACCAGTCCTCCCTCTGTCATCTGTAGGGGACAGGTACCC 60
Db 36 GACATCCAGATCACCAGTCCTCCCTCTGTCATCTGTAGGGGACAGGTACCC 95

QY 61 ATCACTTGCGGGGCAAGTCAGACATTAGGTATTATTTAAATTGGTATCAGCAAAACCA 120
Db 96 ATCGTTTGGGGGCAAGTCAGACATTAGGTATTATTTAAATTGGTATCAGCAAAACCA 155

QY 121 GGAAGAAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCRAAGTGGGTCCCATCA 180
Db 156 GGAAGAAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCRAAGTGGGTCCCATCA 215

QY 181 AGGTTTCAGCGGCGAGTGGATCTGGGACAGAGTTTCATC 217
Db 216 AGGTTTCAGCGGCGAGTGGATCTGGGACATATTTCACTC 252

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Search completed: June 19, 2004, 05:41:24
Job time : 1748 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 07:32:38 ; Search time 1845 Seconds
(without alignments)
8316.224 Million cell updates/sec

Title: US-09-019-441A-7_COPY_58_411

Perfect score: 354

Sequence: 1 gaggtgcagctgtgagtc.....tctgtcaccgtctctcca 354

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 3056378

Minimum DB seq length: 0

Maximum DB seq length: 354

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_on.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_scs.*

28: em_un.*

29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	249.4	70.5	348	9	AF471251	AF471251 Homo sapi
2	246.4	69.6	348	9	AB063673	AB063673 Homo sapi
3	245.6	69.4	348	9	U00491	U00491 Human immun
4	242.4	68.5	348	9	AF231396	AF231396 Homo sapi
5	240.8	68.0	348	9	AB021526	AB021526 Homo sapi
6	240.8	68.0	348	9	HSIGHADJ3	X98751 H.sapiens m
7	239.2	67.6	348	9	HS080150	U00150 Human immun
8	238.8	67.5	342	9	AB066982	AB066982 Homo sapi
9	238.6	67.4	342	9	HSVH3183	X62972 H.sapiens r
10	237.6	67.1	345	9	HSU80154	U00154 Human immun
11	237.4	67.1	348	6	AX112674	AX112674 Sequence
12	236.6	66.8	351	6	AX474084	AX474084 Sequence
13	235.2	66.7	348	9	AF231402	AF231402 Homo sapi
14	235.2	66.4	348	9	AB063899	AB063899 Homo sapi
15	235.2	66.4	348	9	AB066979	AB066979 Homo sapi
16	234.4	66.2	345	9	AF471477	AF471477 Homo sapi
17	234.4	66.2	348	9	AF471559	AF471559 Homo sapi
18	234.4	66.2	348	9	AF471587	AF471587 Homo sapi
19	234.4	66.2	348	9	HSAS56719	AJ556719 Homo sapi
20	233.6	66.0	348	6	AX112744	AX112744 Sequence
21	233.6	66.0	354	9	AB063699	AB063699 Homo sapi
22	233.4	65.9	348	9	AF471241	AF471241 Homo sapi
23	233.4	65.9	348	9	AF471245	AF471245 Homo sapi
24	232.8	65.8	346	9	AY055481	AY055481 Homo sapi
25	232.8	65.8	348	6	AX112640	AX112640 Sequence
26	232.8	65.8	348	9	HSAS238037	AJ238037 Homo sapi
27	232.8	65.8	354	9	AF398962	AF398962 Homo sapi
28	232.6	65.7	351	9	AF004324	AF004324 Homo sapi
29	232.2	65.5	345	9	S71447	S71447 Ig VH (Ig V
30	231.6	65.4	333	9	AF174100	AF174100 Homo sapi
31	231.6	65.4	342	9	AF396476	AF396476 Homo sapi
32	231.2	65.3	345	9	HSAA10305	AJ410905 Homo sapi
33	231.2	65.3	348	9	HSAS56718	AJ556718 Homo sapi
34	230.4	65.1	349	6	AX112726	AX112726 Sequence
35	230.2	65.0	351	9	AB066881	AB066881 Homo sapi
36	230.2	65.0	335	9	AF174105	AF174105 Homo sapi
37	229.6	64.9	348	12	AY180097	AY180097 Synthetic
38	229.6	64.9	349	9	HOMVH3S	D83693 Human mRNA
39	229.6	64.9	354	9	AF455546	AF455546 Homo sapi
40	228.6	64.6	351	6	AX339676	AX339676 Sequence
41	228.6	64.4	348	9	AF471377	AF471377 Homo sapi
42	228.6	64.4	354	9	HSAS298611	AJ298611 Homo sapi
43	227.8	64.4	342	9	HSVH3RG1A	X70468 H.sapiens D
44	227.2	64.2	339	9	HSIHCVD3	X99354 H.sapiens m
45	227.2	64.2	345	9	AB063896	AB063896 Homo sapi

ALIGNMENTS

RESULT 1	AF471251	348 bp	mRNA	linear	PRI 11-OCT-2003
LOCUS	Homo sapiens clone 56-58a Ig heavy chain variable region, VH3				
DEFINITION	Family mRNA, partial cds.				
ACCESSION	AF471251				
VERSION	AF471251.1	GI:33319045			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 348)				
	Scamurri,R.W., Nelson,D.B., Miller,D.J., Lorenz,E. and Janoff,E.N.				
	Impact of HIV-1 on Somatic Hypermutation in Mucosal B Cells				

Pred. No. is the number of results predicted by chance to have a

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Scamurra,R.W., Nelson,D.B., Miller,D.J., Lorenz,E. and Janoff,E.N.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-2002) Division of Infectious Diseases- 111F,
Mucosal and Vaccine Research Center, Veterans Affairs Medical
Center, One Veterans Drive, Minneapolis, MN 55417, USA
FEATURES
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ORIGIN
Query Match 70.5%; Score 249.4; DB 9; Length 348;
Best Local Similarity 83.9%; Pred. No. 3.4e-56;
Matches 296; Conservative 0; Mismatches 51; Indels 6; Gaps 1;
Qy 2 AGGTGACGCTGGTGGAGCTTGGGGCGGCTTGGCAAGCTGGGGGTCCTCGAGACTCT 61
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Qy 62 CCTGGCAGCTCCGGGTTTCCAGTTTCACTTCAATCTACTACTACTACTACTACTACT 121
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Qy 122 AGGTCCAGGCGAGGGCTGGAGTGGGTTCTCAGCTATTAGTAGTGGTGGTATCCACAT 181
Db 116 AGGTCCAGGCGAGGGCTGGAGTGGGTTTATATACATTAGTAGTGGTGGTATCCAT 175
Qy 182 GGTACGACGACTCGTGAAGGCGGATTCACCTCCAGAGAGAGCCCAACACAC 241
Db 176 TCTACGACGACTCTGTGAAGGCGGATTCACCTCCAGGAGCAAGCCCAAGACTCAC 235
Qy 242 TGTTCCTTCAAAATGAACAGAGCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGCGAGCT 301
Db 236 TGTATCTGCAATGAACAGAGCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGCGAG 295
Qy 302 TGACTACAGGCTCTGACTCTGGGGCCAGGAGTCTGTGTCACGGTCTCTCA 354
Db 296 CAAGCCCTACTTTGACTACTGTGGGCCAGGGAACCCCTGGTCCAGCTCTCTCA 348
RESULT 2
AB063673
LOCUS Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
DEFINITION partial cds, clone:H23.
ACCESSION AB063673
VERSION AB063673.1 GI:21668547
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
TITLE Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Kurosawa,Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University,
Kutsukake-cho, Toyosake 470-1192, Japan
{E-mail:kurosawa@fujita-hu.ac.jp, tel:81-562-93-9387}
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/
FEATURES
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ORIGIN
Query Match 69.6%; Score 246.4; DB 9; Length 348;
Best Local Similarity 83.7%; Pred. No. 2.1e-55;
Matches 293; Conservative 0; Mismatches 51; Indels 6; Gaps 1;
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Qy 61 TCTCTGCGAGCTCCGGGTTTCCAGTTTCACTTCAATACTACTACTACTACTACTACT 120
Db 61 TCTCTGCGAGCTCTG-----GATTCACCTTCAGTATTGAAATGAAGTGGTCCGC 114
Qy 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTTCTCACGTATTAGTAGTGGTATCCACA 180
Db 115 CAGGCTCCAGGCGAGGGCTGGAGTGGGTTTATACATTAGTAGTGGTATCCATA 174
Qy 181 TGGTACGACGACTCCGTGAAGGGCAGATTTCACCATCTCCAGAGAGAACGCCAACAC 240
Db 175 TACTACGACGACTCTGTGAAGGCCGATTCACCATCTCCAGAGACACGCCAAGACTCA 234
Qy 241 CTGTTTCCTTCAAAATGAACAGAGCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGCGAGC 300
Db 235 CTGTATCTGCAAAATGAACAGAGCTGAGAGCGCGGACAGCGGTGTCTATTACTGTGCGAGA 294
Qy 301 TTGACTACAGGCTCTGACTCTCTGGGGCCAGGAGTCTCTGGTCCACCGTCTC 350
Db 295 GGTGGGGGAACCTTGTACTACTGTGGGCCAGGGAACCCCTGGTCCACCGTCTC 344
RESULT 3
U00491
LOCUS Human immunoglobulin heavy chain variable region (clone Amuic3-3)
DEFINITION

mRNA, partial cds.
U00491
VERSION
U00491.1 GI:392577
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 348)
Huang, C. and Stollar, B.D.
A majority of Ig H chain cDNA of normal human adult blood
lymphocytes resembles cDNA for fetal Ig and natural autoantibodies
J. Immunol. 151 (10), 5290-5300 (1993)
JOURNAL
MEDLINE
94044753
PUBMED
8228225
REFERENCE
2 (bases 1 to 348)
Stollar, B.D.
Direct Submission
TITLE
Submitted (10-AUG-1993) Stollar B.D., Tufts University,
Biochemistry, 136 Harrison Ave., Boston, MA 02111, USA
JOURNAL
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="Amulc3-3"
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HDYWGQGTLVTVSS"
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Best Local Similarity 83.1%; Pred. No. 3.5e-55;
Matches 294; Conservative 0; Mismatches 54; Indels 6; Gaps 1;
QY 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCTCCGGGTTCCAGTTTCACCTTCAATAACTACTACAGTGGGTCCGC 120
DB 61 TCCTGTCAGCTC-----TAGATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTATCCCA 180
DB 115 CAGGCTCCAGGAGAGGGGCTGGAGTGGGTCTCAGCTATCAGTGGTAGTGGTAGCACA 174
QY 181 TGGTAGCGAGCTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
DB 175 TACTACGAGACTCCGTGAAGGCGCGGTTCCACCATCTCCAGAGACAAATCCAGAACACG 234
QY 241 CTGTTTCTTCAATGAACAGCTGAGAGTGGAGCAGCGCTGTCTATTACTGTGCGAGC 300
DB 235 CTGTATCTGCAATGAACAGCTGAGAGCCGAGGACACCGCCGTATATTACTGTGCGATG 294
QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGAGTCCCTGTCACCGTCTCTCTCA 354
DB 295 GTGGGAGCTTCCCATGACTACTGGGGCCAGGAAACCCCTGTCACCGTCTCTCTCA 348
RESULT 4
AF231396
LOCUS
AF231396 348 bp mRNA linear PRI 13-JUN-2000

mRNA, partial cds.
AF231396
VERSION
AF231396.1 GI:8489278
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 348)
Glas, A.M., van Montfort, B.H.N., Storek, J., Green, E.N.,
Drissen, R.P., Bechtold, V.J., Reilly, J.Z., Dawson, M.A., and
Milner, E.C.B.
B cell-autonomous somatic mutation deficit following bone marrow
transplant
Unpublished
2 (bases 1 to 348)
Glas, A.M. and Milner, E.C.B.
Direct Submission
TITLE
Submitted (07-FEB-2000) Virginia Mason Research Institute, 1201 9th
Ave, Seattle, WA 98101, USA
JOURNAL
FEATURES
Location/Qualifiers
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Best Local Similarity 82.5%; Pred. No. 2.5e-54;
Matches 292; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
QY 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCTCCGGGTTCCAGTTTCACCTTCAATAACTACTACAGTGGGTCCGC 120
DB 61 TCCTGTCAGCTC-----GATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTATCCCA 180
DB 115 CAGGCTCCAGGAGAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTAGCACA 174
QY 181 TGGTAGCGAGCTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
DB 175 TACTACGAGACTCCGTGAAGGCGCGGTTCCACCATCTCCAGAGACAAATCCAGAACACG 234
QY 241 CTGTTTCTTCAATGAACAGCTGAGAGTGGAGCAGCGCTGTCTATTACTGTGCGAGC 300
DB 235 CTGTATCTGCAATGAACAGCTGAGAGCCGAGGACACCGCCGTATATTACTGTGCGAAA 294
QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGAGTCCCTGTCACCGTCTCTCTCA 354
DB 295 CGGATACAGCTATGGGGGTCTGGGGCCAGGAAACCCCTGGTCACTGTCTCTCTCA 348
RESULT 5
AB021526

LOCUS AB021526 348 bp mRNA linear PRI 27-MAR-2002
DEFINITION Homo sapiens mRNA for immunoglobulin heavy chain variable region (IGH), partial cds, clone krpbc21.
ACCESSION AB021526
VERSION AB021526.1 GI:4107065
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Hakoda M., Taniguchi, A., Kotake, S., Higami, K., Ichikawa, N., Silverman, G.J. and Kamatani, N.
AUTHORS Pathogenic implication of a prototype B cell superantigen, staphylococcal protein A, in rheumatoid arthritis
TITLE Unpublished
JOURNAL 2 (bases 1 to 348)
REFERENCE Hakoda M.
AUTHORS Direct Submission
TITLE Submitted (18-DEC-1998) Masayuki Hakoda, Tokyo Women's Medical University, Institute of Rheumatology; 10-22 Kawada-cho Shinjuku-ku, Tokyo 162-0054, Japan
JOURNAL (E-mail: ratokyomomo.so-net.or.jp, Tel: 81-3-5269-1725, Fax: 81-3-5269-1726)
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Query Match 68.0%; Score 240.8; DB 9; Length 348;
Best Local Similarity 82.2%; Pred. No. 6.9e-54;
Matches 291; Conservative 0; Mismatches 57; Indels 6; Gaps 1;
QY 1 GAGGTGCAGCTGTGGAGTCTGGGGGGCTTGGCAAGCTTGGGGGTCCTGAGACTC 60
DB 1 GAGGTGCAGCTGTGGAGTCTGGGGGGCTTGGTACAGCTGGGGGTCCTTAAACTC 60
QY 61 TCCTGGCAGCTCCGGGTCAGGTTCACTTCAATTAATACTATGAGACTGGGTCGC 120
DB 61 TCCTGTGAGGCTCTG-----GATTCACTTTAGCAGCTATGCCATGAGTTGGTCCGC 114
QY 121 CAGGCTCCAGGCGAGGGCTGAGTGGTCTCAAGTATTAGTAGTGGTATGCCACA 180
DB 115 CAGGCTCCAGGAGAGGGCTGAGTGGTCTCAAGTATTAGTGGTATGCCACA 174
QY 181 TGGTACGAGACTCCGTGAAGGGCAGATTCCATCTCCAGAGAACGCCACAACACA 240
DB 175 TACTACGAGACTCCGTGAAGGGCGGTTCACCATCTCCAGAGCAATTCAGAGAAC 234
QY 241 CTGTTTCTTCAATGAACAGCTCAGAGCTCAGGACAGCGCTGTCTATTACTGTGGAGC 300
DB 235 CTGTTATCTGCAATGAACAGCTCAGAGCGCCAGGACAGCGCCGTATTATTACTGTGGAAA 294
QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCAACCGTCTCTCA 354
DB 295 GGGGAACCTGGCTTTGATTACTGGGGCCAGGGAACCTGTGTACCGGTCTCTCA 348
RESULT 6

HSIGHADI3
LOCUS H.sapiens mRNA for variable immunoglobulin heavy chain, clone 3.
DEFINITION X98751
ACCESSION X98751.1 GI:1430804
VERSION X98751.1
KEYWORDS heavy chain; immunoglobulin; variable region.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Dorsam, H., Kipriyanov, S., Welschhof, M. and Little, M.
AUTHORS Isolation of an anti-Digoxigenin antibody out of an human
TITLE IGM-Antibody library and expression in E.coli
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Dorsam, H.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-1996) H. Dorsam, German Cancer Research Center, Diagnostics and Experimental Therapy Program, Recombinant Antibody Group, INF 280, 69120 Heidelberg, FRG
FEATURES source
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misc_feature 1..90
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misc_feature 91..105
/note="CDR1 domain"
misc_feature 106..147
/note="FR2 domain"
misc_feature 148..158
/note="CDR2 domain"
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Query Match 68.0%; Score 240.8; DB 9; Length 348;
Best Local Similarity 82.2%; Pred. No. 6.9e-54;
Matches 291; Conservative 0; Mismatches 57; Indels 6; Gaps 1;
QY 1 GAGGTGCAGCTGTGGAGTCTGGGGGGCTTGGCAAGCTTGGGGGTCCTGAGACTC 60
DB 1 GAGGTGCAGCTGTGGAGTCTGGGGGGCTTGGTACAGCTGGGGGTCCTTAAACTC 60
QY 61 TCCTGGCAGCTCCGGGTCAGGTTCACTTCAATTAATACTATGAGACTGGGTCGC 120
DB 61 TCCTGTGAGGCTCTG-----GATTCACTTTAGCAGCTATGCCATGAGTTGGTCCGC 114
QY 121 CAGGCTCCAGGCGAGGGCTGAGTGGTCTCAAGTATTAGTAGTGGTATGCCACA 180


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DYWGQGTLTVSS"

ORIGIN
Query Match      67.1%; Score 237.6; DB 9; Length 345;
Best Local Similarity 83.6%; Pred. No. 5e-53;
Matches 296; Conservative 0; Mismatches 49; Indels 9; Gaps 2;

QY 1 GAGGTCCAGCTGGTGGAGTCTGGGGCGGGTGGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTCCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60

QY 61 TCGTGGCGAGCCTCCGGGTTCAGGTTTCACGTTCAATPACTACTACATGAGCTGGGTCCGC 120
DB 61 TCGTGGCGAGCCTATG-----GATTCACCTTCAGTGACTACTACATGAGCTGGATCCGCC 115

QY 121 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCACGTTATTAGTAGTGGTATCCCA 180
DB 121 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCACGTTATTAGTAGTGGTATCCCA 180

QY 115 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCACGTTATTAGTAGTGGTATCCCA 174
DB 115 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCACGTTATTAGTAGTGGTATCCCA 174

QY 181 TGGTACGAGACTCCGTGAGGGGAGATTACACCTTCCAGAGAGAGCCCAACACACA 240
DB 181 TGGTACGAGACTCCGTGAGGGGAGATTACACCTTCCAGAGAGAGCCCAACACACA 240

QY 175 TACTACGAGACTCTGTGAGGGGCGGATTACACCTTCCAGGGAGACCCCAAGACTCA 234
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QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTATCTGTGGAGC 300
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QY 235 CTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTATTATCTGTGCAAGA 294
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RESULT 13
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LOCUS      AX474084      351 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 18 from Patent WO0234886.
ACCESSION  AX474084
VERSION     AX474084.1  GI:22208233
KEYWORDS   . synthetic construct
           . synthetic construct
           . artificial sequences.
SOURCE      Chen, G., Hayhurst, A., Thomas, J. G., Iverson, B. L. and Georgiou, G.
ORGANISM   Isolation of binding proteins with high affinity to ligands
           Patent: WO 0234886-A 18 02-MAY-2002;
           Board of Regents, The University of Texas System (US)
           Location/Qualifiers
FEATURES             1..351
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Query Match      66.8%; Score 236.6; DB 6; Length 351;
Best Local Similarity 83.6%; Pred. No. 9.2e-53;
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QY 1 GAGGTCCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 60
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QY 61 TCCTGGCGAGCCTCCGGGTTCAGGTTTCACCTTCAATAACTACTACATGAGCTGGGTCCGC 120
DB 61 TCCTGGCGAGCCTCTG-----GATTCACCTTCAGTGACTACTACATGAGCTGGATCCGC 114

QY 121 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCACGTTATTAGTAGTGGTATCCCA 180
DB 121 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCACGTTATTAGTAGTGGTATCCCA 180

QY 115 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCACGTTATTAGTAGTGGTATCCCA 174
DB 115 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCACGTTATTAGTAGTGGTATCCCA 174

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DB 181 TGGTACGAGACTCCGTGAGGGGAGATTACACCTTCCAGAGAGAGCCCAACACACA 240

QY 175 TACTACGAGACTCTGTGAGGGGCGGATTACACCTTCCAGGGAGACCCCAAGACTCA 234
DB 175 TACTACGAGACTCTGTGAGGGGCGGATTACACCTTCCAGGGAGACCCCAAGACTCA 234

QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTATCTGTGGAGC 300
DB 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTATCTGTGGAGC 300

QY 235 CTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTATTATCTGTGCAAGA 294
DB 235 CTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTATTATCTGTGCAAGA 294

QY 301 TTG---ACTACAGGCTGACTCTCGGGGCCAGGAGTCTCTGGTCCACCGTCTC 350
DB 295 ACGGGTTTCCGGGGTTTGACTATTGGGGGCCAAGGTACCCCTGGGTCAACCGTCTC 347

RESULT 13
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AX112674
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DEFINITION Sequence 155 from Patent WO0127279.
ACCESSION  AX112674
VERSION     AX112674.1  GI:13939321
KEYWORDS   . Homo sapiens (human)
           . Homo sapiens
           . Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           . Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
SOURCE      Edwards, B. M., Main, S. H. and Vaughan, T. J.
ORGANISM   Human anti-adipocyte monoclonal antibodies and their use
           Patent: WO 0127279-A 155 19-APR-2001;
           Cambridge Antibody Technology (GB)
           Location/Qualifiers
FEATURES             1..348
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ORIGIN
Query Match      67.1%; Score 237.4; DB 6; Length 348;
Best Local Similarity 82.2%; Pred. No. 5.6e-53;
Matches 287; Conservative 0; Mismatches 56; Indels 6; Gaps 1;

QY 2 AGGTGAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTCT 61
DB 2 AGGTGAGCTGGTGGAGTCTGGGGGGCGGCTTGGTCAAGCCTGGAGGGCCCTGAGACTTT 61

QY 62 CCGCGCAGCCTCCGGGTTCCAGGTTTCACCTTCAATTAATCTACTACATGGAGCTGGGTCCGC 121
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AF231402      354 bp      mRNA      linear      PRI 13-JUN-2000
LOCUS      Homo sapiens clone 4-4 immunoglobulin heavy chain variable region
DEFINITION      mRNA, partial cds.
ACCESSION      AF231402
VERSION      AF231402.1 GI:8489289
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 354)
AUTHORS      Glas, A.M., van Montfort, E.H.N., Storek, J., Green, E.N., and
Drissen, R.P., Bechtold, V.J., Reilly, J.Z., Dawson, M.A., and
Milner, E.C.B.
TITLE      B cell-autonomous somatic mutation deficit following bone marrow
transplant
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 354)
AUTHORS      Glas, A.M. and Milner, E.C.B.
TITLE      Direct Submission
JOURNAL      Submitted (07-FEB-2000) Virginia Mason Research Institute, 1201 9th
Ave, Seattle, WA 98101, USA
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     /clone="4-4; bml8f61c7"
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ORIGIN
Query Match      66.7%; Score 236; DB 9; Length 354;
Best Local Similarity 82.8%; Pred. No. 1.3e-52;
Matches 298; Conservative 0; Mismatches 50; Indels 12; Gaps 2;

QY      1  GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCTTGAGACTC 60
DB      1  GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGTACAGCCCTGGGGGTCCTTGAGACTC 60

QY      61  TCTGTGGCAGCTCCGGGTTCAAGTTTCACCTTCAATAACTACTACATGAGACTGGTCCGC 120
DB      61  TCTGTGGCAGCTCTG-----GATTACCTTTAGCAGCTATGCCATGAGCTGGTCCGC 114

QY      121  CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCAGTTAGTAGTAGTAGTAGTGGTATCCCA 180
DB      121  CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCAGTTAGTAGTAGTAGTAGTGGTATCCCA 180

QY      115  CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCAGTTAGTAGTAGTAGTAGTGGTATCCCA 174
DB      115  CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCAGTTAGTAGTAGTAGTAGTGGTATCCCA 174

QY      181  TGGTAGCAGACTCCGGTGAAGGCGCAGATTCAACATCTCCAGAGAGAACGCCAACACACA 240
DB      181  TGGTAGCAGACTCCGGTGAAGGCGCAGATTCAACATCTCCAGAGAGAACGCCAACACACA 240

QY      175  TACTAGCAGACTCCGGTGAAGGCGCGTTCAACATCTCCAGAGAGAACATTCCAAAGAACAG 234
DB      175  TACTAGCAGACTCCGGTGAAGGCGCGTTCAACATCTCCAGAGAGAACATTCCAAAGAACAG 234

QY      241  CTGTTTCTTCAATGAAGCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTGCGAGC 300
DB      241  CTGTTTCTTCAATGAAGCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTGCGAGC 300

QY      235  CTGTATCTGCAATGAAGCTGAGAGCTGAGGACAGCGCGCTATATTACTGTGCGAGC 294
DB      235  CTGTATCTGCAATGAAGCTGAGAGCTGAGGACAGCGCGCTATATTACTGTGCGAGC 294

QY      301  TTGACTAC-----AGGGCTCTGACTCTGGGGCCAGGAGTCTCTGTGTCACCGCTCTCTCA 354
DB      301  TTGACTAC-----AGGGCTCTGACTCTGGGGCCAGGAGTCTCTGTGTCACCGCTCTCTCA 354

QY      295  CGTCCCACCTTGGGAGCTACTGGCTACTTGGGGCCAGGAGAACCTGTGTCACTCTCTCA 354
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RESULT 14

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AB063899      348 bp      mRNA      linear      PRI 02-JUL-2002
LOCUS      Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
DEFINITION      partial cds, clone:H249.
ACCESSION      AB063899
VERSION      AB063899.1 GI:21668999
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,
Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,
Mura, K. and Kurosawa, Y.
TITLE      Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 348)
AUTHORS      Kurosawa, Y.
TITLE      Direct Submission
JOURNAL      Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University,
Kutsukake-cho, Toyooka 470-1192, Japan
(S-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             source
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ORIGIN
Query Match      66.4%; Score 235.2; DB 9; Length 348;
Best Local Similarity 81.7%; Pred. No. 2.2e-52;
Matches 286; Conservative 0; Mismatches 58; Indels 6; Gaps 1;

QY      1  GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCTTGAGACTC 60
DB      1  GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGTCCAGCCTGGGGGTCCTTGAGACTC 60

QY      61  TCCTGGCAGCTCCGGGTTCAAGTTTCACCTTCAATAACTACTACATGAGCTGGTCCGC 120
DB      61  TCCTGGTTCAGCCTCTG-----GATTACCTTTCAGTAGCTATGCTATGCTGGGTCCGC 114

QY      121  CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCAGTTAGTAGTAGTAGTAGTGGTATCCCA 180
DB      121  CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCAGTTAGTAGTAGTAGTAGTGGTATCCCA 180

QY      115  CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCAGTTAGTAGTAGTAGTAGTGGTATCCCA 174
DB      115  CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCAGTTAGTAGTAGTAGTAGTGGTATCCCA 174

QY      181  TGGTAGCAGACTCCGGTGAAGGCGCAGATTCAACATCTCCAGAGAGAACGCCAACACACA 240
DB      181  TGGTAGCAGACTCCGGTGAAGGCGCAGATTCAACATCTCCAGAGAGAACGCCAACACACA 240

QY      175  TACTAGCAGACTCCGGTGAAGGCGCAGATTCAACATCTCCAGAGAGAACATTCCAAAGAACAG 234
DB      175  TACTAGCAGACTCCGGTGAAGGCGCAGATTCAACATCTCCAGAGAGAACATTCCAAAGAACAG 234

QY      241  CTGTTTCTTCAATGAAGCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTGCGAGC 300
DB      241  CTGTTTCTTCAATGAAGCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTGCGAGC 300
```

Db 235 CTGTATCTTCAATGAGAGCTGTGAGAGCTGAGACACGGCTGTGTATTACTGTGTGAA 294

Qy 301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCTGGTCACCGTCTC 350

Db 295 AGTCGGGGTTTCTTTGACTACTGGGGCCAGGGAAACCCCTGGTCACCGTCTC 344

RESULT 15

AB066979

LOCUS

DEFINITION

AB066979

VERSION

KEYWORDS

SOURCE

ORGANISM

AB066979 351 bp mRNA linear PRI 02-JUL-2002

Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,

partial cds, clone: a1ms0017h.

AB066979

AB066979.1 GI:21670014

Homo sapiens (human)

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Akatori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,

Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,

Miura, K. and Kurosawa, Y.

Construction and characterization of antibody libraries: isolation

of therapeutic human antibodies and application to functional

genomics

Unpublished

2 (bases 1 to 351)

Kurosawa, Y.

Direct Submission

Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for

Comprehensive Medical Science, Fujita Health University,

Immunology; Kutsukake-cho, Toyosake, Aichi 470-1192, Japan

(E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)

Please visit our web site

URL: <http://www.fujita-hu.ac.jp/immunity/>.

FEATURES

source

1..351

/organism="Homo sapiens"

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/db_xref="taxon:9606"

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/clone_lib="AIMS4"

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ORIGIN

Query Match 66.4%; Score 235; DB 9; Length 351;

Best Local Similarity 83.3%; Pred. No. 2.5e-52;

Matches 294; Conservative 0; Mismatches 50; Indels 9; Gaps 2;

Qy 1 GAGGTGAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAGCGCTGGGGGTCCCTCAGACTC 60

Db 1 GAGGTACAGCTGGTGGAGTCTGGGGGAGGGGTGGTCCAGCTGGGAGTCCCTCAGACTC 60

Qy 61 TCCTGCGAGCCTCGGGTTCAGGTTCACTTCAATAACTACTACATGGAATGGTCCGC 120

Db 61 TCCTGTGAGCCTCTG-----GATTCACCTTCAGTAGCTATAGCAATGAATGGTCCGC 114

Qy 121 CAGGCTCCAGGGCAGGGCTGGAGTGGTCTCAGGTATTAGTAGTAGTATGATCCACCA 180

Db 115 CAGGCTCCAGGGAGGGGCTGGAGTGGTCTCATCCATTAGTAGTAGTAGTACATA 174

181 TGGTACGCACTCGTGGTGAAGGGCAGATTCCACCATCTCCAGAGAGAACGCCAACACACA 240

175 TACTACGCACTCAGTGAAGGGCCGATTCCACCATCTCCAGAGAGAACGCCAAGAACTCA 234

241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACAGGCTGTCTATTACTGTGGAGC 300

235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 294

301 TTGACTACAGGGTCTG---ACTCTCTGGGGCCAGGGAGTCTGGTCAACCGTCTC 350

295 GATATAGCAGCAGCTGGTAACTACTTGGGGCCAGGGAAACCCCTGGTCAACCGTCTC 347

Search completed: June 19, 2004, 08:52:20

Job time : 1848 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 07:31:37 ; Search time 280 Seconds
(without alignments)
5370.936 Million cell updates/sec

Title: US-09-019-441A-7_COPY_58_411
Perfect score: 354
Sequence: 1 gagtgccagcggggagtc.....tcctggtcacgcgtctctcca 354

Scoring table: IDENTITY NUC
Gapop 10.0 ; Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 4221282

Minimum DB seq length: 0
Maximum DB seq length: 354

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:*
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2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	247.2	69.8	348	6 AAL39119	Antibody
2	241.6	68.2	348	6 AAD46290	Human KDR
3	241.6	68.2	348	7 ABT23325	VEGF bind
4	241.6	68.2	348	9 ADD24416	Human hea
5	241.6	68.2	348	9 ADD80793	Human cto
6	240	67.8	348	6 AAD46292	Human KDR
7	240	67.8	348	7 ABT23327	VEGF bind
8	240	67.8	348	9 ADD24420	Human hea
9	240	67.8	348	9 ADD80797	Human cto
10	238.4	67.3	348	6 AAD46294	Human KDR
11	238.4	67.3	348	7 ABT23329	VEGF bind
12	238.4	67.3	348	9 ADD24423	Human hea
13	238.4	67.3	348	9 ADD80800	Human cto
14	237.4	67.1	348	4 AAS03478	DNA encod
15	236.6	66.8	351	6 AAL43586	Dig3 anti
16	233.6	66.0	348	4 AAS03513	DNA encod
17	232.8	65.8	348	4 AAS03461	DNA encod
18	232.6	65.7	351	6 ABK90972	Human ant
19	230.4	65.1	349	4 AAS03504	DNA encod
20	228.6	64.6	351	6 ABA92717	Fibronect
21	226.4	64.0	354	4 AAS03470	DNA encod
22	223.8	63.2	354	2 AAT72127	CEA-speci
23	223.2	63.1	354	2 AAT72128	CEA-speci

24	223	63.0	348	4 AAS03446	DNA encod
25	222.6	62.9	294	7 ACC00475	Human ger
26	222.6	62.9	311	4 ABS46318	Human liv
27	222.6	62.9	311	6 ABS20923	Human gen
28	222.4	62.8	348	2 AAT72130	CBA-speci
29	222.4	62.8	354	4 AAH47513	Anti-IL-1
30	221.6	62.6	294	3 AAZ46860	Human imm
31	221.6	62.6	296	6 ABS62711	Germline
32	221.6	62.6	345	4 AAS03511	DNA encod
33	221	62.4	294	7 ACC00478	Human ger
34	220.4	62.3	339	3 AAZ27658	DNA encod
35	219	61.9	348	6 ABA94334	MAB 27A1
36	219	61.9	354	3 AAC96948	Human ant
37	218.4	61.7	345	6 ABA94332	MAB 12B5
38	218.2	61.5	351	6 ABA94338	MAB 63 he
39	217.8	61.5	294	3 AAZ46861	Human imm
40	217.4	61.4	336	3 AAZ27662	DNA encod
41	216.8	61.2	296	6 ABS62712	Germline
42	215.8	61.0	354	7 AAD45588	Human VEG
43	215.6	60.9	351	6 ABK88457	Human ant
44	215.4	60.8	351	2 AAG64850	SpA-react
45	214.4	60.6	342	4 AAF29060	Human HIV

ALIGNMENTS

RESULT 1
AAL39119
ID AAL39119 standard; DNA; 348 BP.
XX
AC AAL39119;
XX
DT 02-SEP-2002 (first entry)
XX
DE Antibody screening method related DNA VH(DP-47).
XX
KW Screening antibody; 2-D electrophoresis; plural protein; protein spot;
XX antibody library; proteomics; ds.
XX Unidentified.
XX WO200242774-A1.
XX 30-MAY-2002.
XX
XX PF 05-JUN-2001; 2001WO-JP004732.
XX
XX PR 24-NOV-2000; 2000JP-00358539.
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX (NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.
XX Kaneko K;
XX
XX WPI; 2002-471742/50.
XX P-PSDB; AAO21548.
XX
XX Screening an antibody using 2-D electrophoresis on plural proteins in
samples for separating individual protein spots to react with an antibody
library useful in proteomics and other biological sciences.
XX
XX Disclosure; Fig 1; 78pp; Japanese.
XX
XX The invention relates to a novel method for screening an antibody,
comprising performing 2-D electrophoresis on plural proteins in a sample.
XX Individual protein spots are separated by reacting them with an antibody
library and then replicating the bound antibodies before reacting them
XX with the spot proteins again. The method is useful for screening an
antibody specific for a target protein, e.g. from a phage antibody
XX library, which is useful in proteomics for studying various protein and
complementary deoxyribonucleic acid (cDNA) expression libraries as well
XX as gene functions, and in other biological and medical sciences. This

CC polynucleotide is a DNA sequence relating to the antibody screening
 CC method of the invention
 XX
 SQ Sequence 348 BP; 71 A; 84 C; 108 G; 73 T; 0 U; 12 Other;
 Query Match 69.8%; Score 247.2; DB 6; Length 348;
 Best Local Similarity 82.6%; Pred. No. 5.4e-59;
 Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
 QY 1 GAGGTGACGCTGTGGAGTCTGGGGGGGCTTGGCAAGGCTGGGGGGTCCCTGAGACTC 60
 DB 1 GAGGTGACGCTGTGGAGTCTGGGGGGGCTTGGCAAGGCTGGGGGGTCCCTGAGACTC 60
 QY 61 TCCGTGCGAGCTCCGGGTTCCAGTTTCACTTCAATTAACCTACTACATGGACTGGTCCGC 120
 DB 61 TCCGTGCGAGCTCTG-----GATTACCTTTAGAGCTATGCCATGAGCTGGGTCCGC 114
 QY 121 CAGGCTCAGGCGAGGGCTGAGTGGTCTCAGTATTAGTAGTATGTTGATGCCACA 180
 DB 115 CAGGCTCAGGCGAGGGCTGAGTGGTCTCAGTATTAGTAGTATGTTGATGCCACA 174
 QY 181 TGGTACGAGACTCCGTGAGGGGAGATTCCACCATCTCCAGAGAGAACGCCAACACACA 240
 DB 175 TACTACGAGACTCCGTGAGGGGCGGTTCCACCATCTCCAGAGAGAACGCCAACACAO 234
 QY 241 CTGTTTCTTCAATGAAACAGCTCAGAGCTGAGACACGGCTGTCTATTACTGTGCGAGC 300
 DB 235 CTGTATCTGCAATGAAACAGCTCAGAGCTGAGACACGGCTGTCTATTACTGTGCGAAA 294
 QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGAGTCTGTGTACCGCTC 350
 DB 295 NNNNNNNNNNTTGTACTACTGGGGCCAGGAAACCTGTGTACCGCTC 344
 RESULT 2
 AAD46290
 ID AAD46290 standard; DNA; 348 BP.
 XX
 AC AAD46290;
 XX
 XX 27-DEC-2002 (first entry)
 XX Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2C6 clone.
 XX
 XX Human; tumour; vascular endothelial growth factor receptor; metastasis;
 XX epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
 XX breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene; VH;
 XX ds.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS 1..348
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 XX /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
 XX protein"
 XX /note= "CDS does not include start and stop codon"
 XX /partial
 XX
 XX WO200270008-A1.
 XX
 XX 12-SEP-2002.
 XX
 XX 04-MAR-2002; 2002WO-US006762.
 XX
 XX 02-MAR-2001; 2001US-00798689.
 XX
 XX (INCL-) INCLONE SYSTEMS INC.
 XX (ROCK/) ROCKWELL P.
 XX (GOLD/) GOLDSTEIN N I.
 XX
 XX WPI; 2002-691738/74.
 XX P-ESDB; AAE28870.

XX Inhibiting tumor growth in humans involves administering vascular
 PT endothelial growth factor receptor antagonists in combination with
 PT radiation, chemotherapeutic agents, or epidermal growth factor receptor
 PT antagonists.
 XX Example 9; Page 121-122; 151pp; English.
 XX The invention relates to a method of inhibiting tumour growth which
 CC involves administering, vascular endothelial growth factor receptor
 CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
 CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
 CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.
 CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
 CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
 CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
 CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour
 CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
 CC It is preferably useful for treating subjects with both solid tumours,
 CC preferably high vascular tumours and non-solid tumours. The inhibition or
 CC reduction of tumour growth includes prevention or inhibition of the
 CC progression of tumour, including cancerous and non-cancerous tumours,
 CC where the progression of tumours includes the invasiveness, metastasis,
 CC recurrence and increase in size of the tumour. The present sequence is
 CC human KDR (VEGFR-2) Fab antibody heavy chain DNA
 XX
 SQ Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
 Query Match 68.2%; Score 241.6; DB 6; Length 348;
 Best Local Similarity 82.9%; Pred. No. 2e-57;
 Matches 290; Conservative 0; Mismatches 54; Indels 6; Gaps 1;
 QY 1 GAGGTGACGCTGTGGAGTCTGGGGGGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
 DB 1 GAGGTGACGCTGTGGAGTCTGGGGGGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
 QY 61 TCCGTGCGAGCTCCGGGTTCCAGTTTCACTTCAATTAACCTACTACATGAGCTGGGTCCGC 120
 DB 61 TCCGTGCGAGCTCTG-----GATTACCTTTAGAGCTATGAGTATGATGCCACA 114
 QY 121 CAGGCTCAGGCGAGGGCTGAGTGGTCTCAGTATTAGTAGTATGATGCCACA 180
 DB 115 CAGGCTCAGGCGAGGGCTGAGTGGTCTCAGTATTAGTAGTATGATGCCACA 174
 QY 181 TGGTACGAGACTCCGTGAGGGGAGATTCCACCATCTCCAGAGAGAACGCCAACACACA 240
 DB 175 TACTACGAGACTCAGTGAAGGGCCGATTCAACATCTCCAGAGAGAACGCCAACACTCA 234
 QY 241 CTGTTTCTTCAATGAAACAGCTCAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
 DB 235 CTGTATCTGCAATGAAACAGCTCAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGA 294
 QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGAGTCTGTGTACCGCTC 350
 DB 295 GTCACAGATGCTTTTGTATCTATCTGGGGCCAGGAGCAATGTTCCCGTCTC 344
 RESULT 3
 ABT23325
 ID ABT23325 standard; DNA; 348 BP.
 XX
 AC ABT23325;
 XX
 XX 01-MAY-2003 (first entry)
 XX
 XX VEGF binding related DNA SEQ ID No 75.
 XX
 XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
 XX leukaemia cell; vascular endothelial growth factor; tumour;
 XX bispecific antigen-binding protein; human; gene; db.
 XX
 XX Homo sapiens.

PN W02003002144-A1.
 XX 09-JAN-2003.
 XX 26-JUN-2002; 2002WO-US020332.
 XX 26-JUN-2001; 2001US-0301299P.
 XX (IMCL-) IMCLONE SYSTEMS INC.
 XX Zhu Z;
 XX WPI; 2003-201468/19.
 DR P-PSDB; ABJ26763.
 XX New bispecific antibodies having antigen-binding sites specific for a
 PT first vascular endothelial growth factor (VEGF) receptor and for a second
 PT VEGF receptor, useful for inhibiting migration of leukemia cells, or for
 PT treating tumors.
 XX Disclosure; Page 70; 98pp; English.
 XX The invention relates to a novel antibody having a first antigen binding
 CC site specific for a first vascular endothelial growth factor (VEGF)
 CC receptor and a second antigen-binding site specific for a second VEGF
 CC receptor. The bispecific antigen-binding proteins block activation of the
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
 CC cellular functions such as mitogenesis of vascular endothelial cells and
 CC migration of leukaemia cells. The antibodies are useful for treating
 CC tumors and for in vivo or in vitro for investigative and diagnostic
 CC methods. This polynucleotide sequence represents a human DNA sequence
 CC relating to the bispecific antibodies that bind to the VEGF receptors of
 CC the invention
 XX
 SQ Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
 Query Match 68.2%; Score 241.6; DB 7; Length 348;
 Best Local Similarity 82.9%; Pred. No. 2e-57;
 Matches 290; Conservative 0; Mismatches 54; Indels 6; Gaps 1;
 QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 60
 DB 1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTGGTCAAGCCTGGGGGGTCCCTGAGACTC 60
 QY 61 TCCTGGCGAGCTCCGGGTTTCAGGTTTCAGCTTCAATTAATACTACTGAGTGGGTCCGC 120
 DB 61 TCCTGTSCAGCCTCTG-----GATTTCACCTTCAGTACGTATGATAGTGTACATA 114
 QY 121 CAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTCAAGTATTAGTAGTGGTGTATCCCA 180
 DB 115 CAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCATCCATTAGTAGTGTATGATAGTGTACATA 174
 QY 181 TGGTACGAGACTCCGTGAGGCGAGATTTCACCATCTCCAGAGAGAGCCCAACACACA 240
 DB 175 TACTACGAGACTCAGTGAAGGCGCATTCACCATCTCCAGAGAGAGCCCAACAGACTCA 234
 QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGTGGAGTGGAGACCGGCTGTCTATTACTGTGCGAGC 300
 DB 235 CTGTATCTGCAATGACAGCCTGAGCGGAGGACACCGGCTGTGTATTACTGTGCGAGA 294
 QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTGTGTCACCGTCTC 350
 DB 295 GTCCACAGATGCTTTTGATATCTGGGGCCAGGGAGCAATGCTCACCGTCTC 344

RESULT 4

ADD24416

ID ADD24416 standard; DNA; 348 BP.

XX AC

XX ADD24416;

XX 15-JAN-2004 (first entry)

DT

DE Human heavy chain variable region DNA #2.
 XX
 KW tumour; vascular endothelial growth factor receptor; VEGFR;
 KW epidermal growth factor receptor; EGFR; cancer; human; ds; gene.
 XX
 CS Homo sapiens.
 XX US2003108545-A1.
 XX 12-JUN-2003.
 XX
 PF 04-MAR-2002; 2002US-00091300.
 XX 10-FEB-1994; 94US-00196041.
 PR 20-OCT-1994; 94US-00326552.
 PR 07-JUN-1995; 95US-00476533.
 PR 03-SEP-1996; 96US-00706804.
 PR 07-JAN-1997; 97US-00779450.
 PR 10-NOV-1997; 97US-00967113.
 PR 22-SEP-1999; 99US-00401163.
 PR 02-MAR-2001; 2001US-00798689.
 XX (ROCK/) ROCKWELL P.
 PA (GOLD/) GOLDSTEIN N I.
 XX
 PI Rockwell P, Goldstein NI;
 XX WPI; 2003-801265/75.
 DR P-PSDB; ADD24417.
 XX
 DR Inhibiting tumor growth by administering to a human a vascular
 PT endothelial growth factor receptor (VEGFR) antagonist and epidermal
 PT growth factor receptor (EGFR) antagonist.
 XX
 PS Example 12; SEQ ID NO 23; 90pp; English.
 XX
 CC The invention relates to a method of inhibiting tumour growth comprising
 CC administering to a human a vascular endothelial growth factor receptor
 CC (VEGFR) antagonist and epidermal growth factor receptor (EGFR)
 CC antagonist. The method is useful for inhibiting tumour growth. The
 CC present sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
 Query Match 68.2%; Score 241.6; DB 9; Length 348;
 Best Local Similarity 82.9%; Pred. No. 2e-57;
 Matches 290; Conservative 0; Mismatches 54; Indels 6; Gaps 1;
 QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 60
 DB 1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTGGTCAAGCCTGGGGGGTCCCTGAGACTC 60
 QY 61 TCCTGGCGAGCTCCGGGTTTCAGGTTTCAGCTTCAATTAATACTACTGAGTGGGTCCGC 120
 DB 61 TCCTGTGAGCCTCTG-----GATTTCACCTTCAGTACGTATGATAGTGTACATA 114
 QY 121 CAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTCAAGTATTAGTAGTGGTGTATCCCA 180
 DB 115 CAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCATCCATTAGTAGTGTATGATAGTGTACATA 174
 QY 181 TGGTACGAGACTCCGTGAGGCGAGATTTCACCATCTCCAGAGAGAGCCCAACACACA 240
 DB 175 TACTACGAGACTCAGTGAAGGCGCATTCACCATCTCCAGAGAGAGCCCAACAGACTCA 234
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 DB 235 CTGTATCTGCAATGACAGCCTGAGCGGAGGACACCGGCTGTGTATTACTGTGCGAGA 294
 QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTGTGTCACCGTCTC 350
 DB 295 GTCCACAGATGCTTTTGATATCTGGGGCCAGGGAGCAATGCTCACCGTCTC 344

RESULT 5
 ADD80793
 ID ADD80793 standard; DNA; 348 BP.
 XX
 AC ADD80793;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human clone D2C6 KDR-binding Fab variable heavy chain gene SEQ ID NO:23.
 XX
 DE human; antibody; KDR; cytostatic; gene therapy; anti-KDR antibody;
 XX
 KW tumour; angiogenesis; gene; ds.
 XX
 OS Homo sapiens.
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 FT /product= "KDR-binding Fab"
 FT /note= "No start/stop codon given"
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 FN WO20003075840-A2.
 XX
 PD 18-SEP-2003.
 XX
 PF 04-MAR-2003; 2003WO-US006459.
 XX
 PR 04-MAR-2002; 2002US-0361783P.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 XX
 FI Zhu Z;
 XX
 WI MPI; 2003-779032/73.
 DR P-PSDB; ADD80794.
 XX
 DE New human anti-KDR antibody, useful for preparing a composition for
 PT reducing tumor growth and inhibiting angiogenesis.
 XX
 PS Claim 11; SEQ ID NO 23; 49pp; English.
 XX
 CC The invention relates to a novel isolated human antibody or its fragment
 CC binds selectively to KDR. An antibody of the invention has cytostatic
 CC activity, and may have a use in gene therapy. The antibody is anti-KDR
 CC antibody. The antibody is useful for preparing a composition for reducing
 CC tumor growth and inhibiting angiogenesis. The present sequence is used
 CC in the exemplification of the invention.
 XX
 SQ Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
 Query Match 68.2%; Score 241.6; DB 9; Length 348;
 Best Local Similarity 82.9%; Pred. No. 2e-57; Mismatches 54; Indels 6; Gaps 1;
 Matches 290; Conservative 0;
 QY 1 GAGGTGCGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 60
 DB |||||
 QY 1 GAGGTGCGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 60
 DB |||||
 QY 61 TCCTGCGAGCTCCGGGTTCAGGTTCACCTTCAATACTACTACATGACTGGTCCGC 120
 DB |||||
 QY 61 TCCTGCGAGCTCCG-----GATTCACCTTCAGTAGCTATAGCATGAATGGGTCCGC 114
 DB |||||
 QY 121 CAGGCTCCAGGCGCAGGCTGGAGTGGGTCTCACTATTAGTAGTGGTATCCACCA 180
 DB |||||
 QY 115 CAGGCTCCAGGCGCAGGCTGGAGTGGGTCTCACTATTAGTAGTGGTATCCACCA 174
 DB |||||
 QY 181 TGGTAGCGAGCTCCGTTAGGCGCAGATTCCATCTCCAGAGAAAGCCCAACACA 240
 DB |||||
 QY 175 TACTACGCGAGCTCAGTGAAGGCGGATTCCATCTCCAGAGAAAGCCCAACACTCA 234
 DB |||||
 QY 241 CTGTTCTCTCAATGAAGCCTGAGCTGAGGACAGGCTGTCTATTACTGTGCGAGC 300
 DB |||||
 QY 235 CTGTATCTGCAATGAAGCCTGAGAGCCGAGACAGGCTGTGTATTACTGTGCGAGA 294
 DB |||||

QY 301 TTGACTACAGGGTCTGACTCTCGGGCCAGGAGTCTGTTGTCACCGTCTC 350
 DB |||||
 QY 295 GTACACAGATGCTTTGATATCTGGGGCCAAAGGACAATGGTCAACCGTCTC 344
 DB |||||
 RESULT 6
 AAD46292
 ID AAD46292 standard; DNA; 348 BP.
 XX
 AC AAD46292;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DE Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from DIH4 clone.
 XX
 DE human; tumour; vascular endothelial growth factor receptor; metastasis;
 KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
 KW breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene; VH;
 XX ds.
 XX OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..348
 FT /*tag= a
 FT /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
 FT protein"
 FT /note= "CDS does not include start and stop codon"
 FT /partial
 XX
 FN WO200270009-A1.
 XX
 PD 12-SEP-2002.
 XX
 PF 04-MAR-2002; 2002WO-US006762.
 XX
 PR 02-MAR-2001; 2001US-00798689.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 PA (ROCK/) ROCKWELL P.
 PA (GOLD/) GOLDSTEIN N I.
 XX
 WI MPI; 2002-691738/74.
 DR P-PSDB; AAE28870.
 XX
 DE Inhibiting tumor growth in humans involves administering vascular
 PT endothelial growth factor receptor antagonists in combination with
 PT radiation, chemotherapeutic agents, or epidermal growth factor receptor
 PT antagonists.
 XX
 Example 12; Page 124-125; 151pp; English.
 XX
 CC The invention relates to a method of inhibiting tumour growth which
 CC involves administering, vascular endothelial growth factor receptor
 CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
 CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
 CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.
 CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
 CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
 CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
 CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour
 CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
 CC It is preferably useful for treating subjects with both solid tumours,
 CC preferably high vascular tumours and non-solid tumours. The inhibition or
 CC reduction of tumour growth includes prevention or inhibition of the
 CC progression of tumour, including cancerous and non-cancerous tumours,
 CC where the progression of tumours includes the invasiveness, metastasis,
 CC recurrence and increase in size of the tumour. The present sequence is
 CC human KDR (VEGFR-2) Fab antibody heavy chain DNA
 XX
 SQ Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 U; 0 Other;

Query Match 67.8%; Score 240; DB 6; Length 348;
Best Local Similarity 82.6%; Pred. No. 5.5e-57;
Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGCGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTCCAGCTGGTGGAGTCTGGGGGAGGCTGGTCAAGCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCTCCGGGTTTCAGGTTCACTTCAATAAAGTCTTACATGAGCTGGGTCCGC 120
DB 61 TCCTGTGCGAGCTCTG-----GATTCACTTTCAGTAGCTATAGCATGAATGGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTTATTAGTAGTAGTGGTATCCACACA 180
DB 115 CAGGCTCCAGGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTATACATA 174
QY 181 TGGTAGCAGACTCCGTGAGGCGCAATTCACCTCTCCAGAGAGAGAGCCCAACACACA 240
DB 175 TACTACGCGAGCTCAGTGAAGGCGCGATTACCATCTCCAGAGACAACGCCCAAGAACTCA 234
QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
DB 235 CTGTATCTGCAANTGAACAGCTGAGAGCGGCTGAGCGAGGACACGGCTGTATTACTGTGCGAGA 294
QY 301 TTGACTACAGGCTCTGACTCTCGGGCGCAGGGAGTCCCTGGTCAACCGTCTC 350
DB 295 GTACAGATGCTTTTGATATCTGGGGCCAAAGGACAATGGTCAACCGTCTC 344

RESULT 7
ABT23327
ID ABT23327 standard; DNA; 348 BP.
XX AC ABT23327;
XX DT 01-MAY-2003 (first entry)
XX DE VEGF binding related DNA SEQ ID No 79.
XX KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
XX KW leukemia cell; vascular endothelial growth factor; tumour;
XX KW bispecific antigen-binding protein; human; gene; ds.
XX OS Homo sapiens.
XX PN W02003002144-A1.
XX PD 09-JAN-2003.
XX PF 26-JUN-2002; 2002WO-US020332.
XX PR 26-JUN-2001; 2001US-0301299P.
XX PA (IMCL-) IMCLONE SYSTEMS INC.
XX PI Zhu Z;
XX PI WPI; 2003-201468/19.
XX PT New bispecific antibodies having antigen-binding sites specific for a
XX PT first vascular endothelial growth factor (VEGF) receptor and for a second
XX PT VEGF receptor, useful for inhibiting migration of leukemia cells, or for
XX PT treating tumors.
XX PS Disclosure; Page 72; 98pp; English.

XX CC The invention relates to a novel antibody having a first antigen binding
XX CC site specific for a first vascular endothelial growth factor (VEGF)
XX CC receptor and a second antigen-binding site specific for a second VEGF
XX CC receptor. The bispecific antigen-binding proteins block activation of the
XX CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
XX CC cellular functions such as mitogenesis of vascular endothelial cells and
XX CC migration of leukaemia cells. The antibodies are useful for treating

CC tumours and for in vivo or in vitro for investigative and diagnostic
CC methods. This polynucleotide sequence represents a human DNA sequence
CC relating to the bispecific antibodies that bind to the VEGF receptors of
CC the invention
XX SQ Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 U; 0 Other;
Query Match 67.8%; Score 240; DB 7; Length 348;
Best Local Similarity 82.6%; Pred. No. 5.5e-57;
Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGCGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTCCAGCTGGTGGAGTCTGGGGGAGGCTGGTCAAGCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCTCCGGGTTTCAGGTTCACTTCAATAAAGTCTTACATGAGCTGGGTCCGC 120
DB 61 TCCTGTGCGAGCTCTG-----GATTCACTTTCAGTAGCTATAGCATGAATGGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTTATTAGTAGTAGTGGTATCCACACA 180
DB 115 CAGGCTCCAGGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTATACATA 174
QY 181 TGGTAGCAGACTCCGTGAGGCGCAATTCACCTCTCCAGAGAGAGAGCCCAACACACA 240
DB 175 TACTACGCGAGCTCAGTGAAGGCGCGATTACCATCTCCAGAGACAACGCCCAAGAACTCA 234
QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
DB 235 CTGTATCTGCAANTGAACAGCTGAGAGCGGCTGAGCGGAGGACACGGCTGTATTACTGTGCGAGA 294
QY 301 TTGACTACAGGCTCTGACTCTCGGGCGCAGGGAGTCCCTGGTCAACCGTCTC 350
DB 295 GTACAGATGCTTTTGATATCTGGGGCCAAAGGACAATGGTCAACCGTCTC 344

RESULT 8
ADD24420
ID ADD24420 standard; DNA; 348 BP.
XX AC ADD24420;
XX DT 15-JAN-2004 (first entry)
XX DE Human heavy chain variable region DNA #3.
XX KW tumour; vascular endothelial growth factor receptor; VEGFR;
XX KW epidermal growth factor receptor; EGFR; cancer; human; ds; gene.
XX OS Homo sapiens.
XX PN US2003108545-A1.
XX PD 12-JUN-2003.
XX PF 04-MAR-2002; 2002US-00091300.
XX PR 10-FEB-1994; 94US-00196041.
XX PR 20-OCT-1994; 94US-00326552.
XX PR 07-JUN-1995; 95US-00476533.
XX PR 03-SEP-1996; 96US-00706804.
XX PR 07-JAN-1997; 97US-00779450.
XX PR 10-NOV-1997; 97US-00967113.
XX PR 22-SEP-1999; 99US-00401163.
XX PR 02-MAR-2001; 2001US-00798689.
XX PA (ROCK/) ROCKWELL P.
XX PA (GOLD/) GOLDSTEIN N I.
XX PI Rockwell P, Goldstein NI;
XX PI WPI; 2003-801265/75.
XX DR P-PSDB; ADD24417.

XX Inhibiting tumor growth by administering to a human a vascular
PT endothelial growth factor receptor (VEGFR) antagonist and epidermal
FT growth factor receptor (EGFR) antagonist.
XX
XX
PS Example 12; SEQ ID NO 27; 90pp; English.
XX
XX The invention relates to a method of inhibiting tumour growth comprising
CC administering to a human a vascular endothelial growth factor receptor
CC (VEGFR) antagonist and epidermal growth factor receptor (EGFR)
CC antagonist. The method is useful for inhibiting tumour growth. The
CC present sequence is used in the exemplification of the invention.
XX
XX
SQ Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 U; 0 Other;
Query Match 67.8%; Score 240; DB 9; Length 348;
Best Local Similarity 82.6%; Pred. No. 5.5e-57;
Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
QY 1 GAGGTGAGCTGGTGGAGTCTGGGGGGGGCTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTCCAGCTGGTGGAGTCTGGGGGGGGCTGGTCAAGCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGAGCTCCGGGTTTCAGGTTTCACCTTCAATAACTACTACATGACTGGGTCCGC 120
DB 61 TCCTGTGAGCTCTG-----GATTCACCTTCAGTACTATAGCATGAATCTGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGTGGAGTGGTCTCACTATAGTAGTGGTGGTCCGC 180
DB 115 CAGGCTCCAGGGCAGGGGTGGAGTGGTCTCACTATAGTAGTGGTGGTCCGC 174
QY 181 TGGTACGAGACTCCGTGAGGGCAGATTCCACCTCCAGAGAGAGCCCAACACACA 240
DB 175 TACTACGAGACTAGTGGAGGGCCGATTCACCTCCAGAGAGAGCCCAAGACTCA 234
QY 241 CTGTTTCTCAATGAACAGCTGAGAGCTGAGAGCAGGGTGTCTATTACTGTGCGAGC 300
DB 235 CTGTTATCTGCAATGAACAGCTGAGAGCCGAGGACAGGGTGTGTTATTACTGTGCGAGA 294
QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCCCTGCTCACCGTCTC 350
DB 295 GTACAGAGATGCTTTTGATATCTGGGGCCAGGGACAAATGGTCCACCGTCTC 344
RESULT 9
ADD80797
ID ADD80797 standard; DNA; 348 BP.
XX
XX
AC ADD80797;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human clone DIH4 KDR-binding Fab variable heavy chain gene SEQ ID NO:27.
XX
XX human; antibody; KDR; cytostatic; gene therapy; anti-KDR antibody;
XX tumour; angiogenesis; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..348
XX /*tag= a
XX /product= "KDR-binding Fab"
XX /note= "No start/stop codon given"
XX
XX WO2003075840-A2.
XX
XX 18-SEP-2003.
XX
XX 04-MAR-2003; 2003WO-US0006459.
XX
XX 04-MAR-2002; 2002US-0361783P.
XX

PA (IMCL-) IMCLONE SYSTEMS INC.
XX
XX
PI Zhu Z;
XX
XX
DR WZi: 2003-779032/73.
DR P-PSDB; ADD80794.
XX
XX New human anti-KDR antibody, useful for preparing a composition for
PT reducing tumor growth and inhibiting angiogenesis.
XX
XX
PS Example 1; SEQ ID NO 27; 49pp; English.
XX
XX The invention relates to a novel isolated human antibody or its fragment
CC binds selectively to KDR. An antibody of the invention has cytostatic
CC activity, and may have a use in gene therapy. The antibody is anti-KDR
CC antibody. The antibody is useful for preparing a composition for reducing
CC tumour growth and inhibiting angiogenesis. The present sequence is used
CC in the exemplification of the invention.
XX
XX
SQ Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 U; 0 Other;
Query Match 67.8%; Score 240; DB 9; Length 348;
Best Local Similarity 82.6%; Pred. No. 5.5e-57;
Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
QY 1 GAGGTGAGCTGGTGGAGTCTGGGGGGGGCTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTCCAGCTGGTGGAGTCTGGGGGGGGCTGGTCAAGCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGAGCTCCGGGTTTCAGGTTTCACCTTCAATAACTACTACATGACTGGGTCCGC 120
DB 61 TCCTGTGAGCTCTG-----GATTCACCTTCAGTACTATAGCATGAATCTGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGTGGAGTGGTCTCACTATAGTAGTGGTGGTCCGC 180
DB 115 CAGGCTCCAGGGCAGGGGTGGAGTGGTCTCACTATAGTAGTGGTGGTCCGC 174
QY 181 TGGTACGAGACTCCGTGAGGGCAGATTCCACCTCCAGAGAGAGCCCAACACACA 240
DB 175 TACTACGAGACTAGTGGAGGGCCGATTCACCTCCAGAGAGAGCCCAAGACTCA 234
QY 241 CTGTTTCTCAATGAACAGCTGAGAGCTGAGAGCAGGGTGTCTATTACTGTGCGAGC 300
DB 235 CTGTTATCTGCAATGAACAGCTGAGAGCCGAGGACAGGGTGTGTTATTACTGTGCGAGA 294
QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCCCTGCTCACCGTCTC 350
DB 295 GTACAGAGATGCTTTTGATATCTGGGGCCAGGGACAAATGGTCCACCGTCTC 344
RESULT 10
AAD46294
ID AAD46294 standard; DNA; 348 BP.
XX
XX
AC AAD46294;
XX
XX 27-DEC-2002 (first entry)
XX
XX Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2H2 clone.
XX
XX Human; tumour; vascular endothelial growth factor receptor; metastasis;
XX epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
XX breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene; VH;
XX ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..348
XX /*tag= a
XX /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
XX protein"
XX /note= "CDS does not include start and stop codon"
XX
XX


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Db 235 CTGTATCTGCAATGAACAGCCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGGAGA 294
QY 301 TTGACTACAGGCTCTGACTCTGGGGCCAGGGAGTCTGTGTACCCCTCTC 350
Db 295 GTACAGATGCTTTTGATATCTGGGGCCAAAGGACAAATGGTCAACCCCTCTC 344

RESULT 12
ID ADD24423 standard; DNA; 348 BP.
AC ADD24423;
XX
XX 15-JAN-2004 (first entry)
XX Human heavy chain variable region DNA #4.
XX
XX tumour; vascular endothelial growth factor receptor; VEGFR;
XX epidermal growth factor receptor; EGFR; cancer; human; ds; gene.
XX
XX Homo sapiens.
XX
XX US2003108545-A1.
XX
XX 12-JUN-2003.
XX
XX 04-MAR-2002; 2002US-00091300.
XX
XX 10-FEB-1994; 94US-00196041.
XX 20-OCT-1994; 94US-00326552.
XX 07-JUN-1995; 95US-00476533.
XX 03-SEP-1996; 96US-00706804.
XX 07-JAN-1997; 97US-00779450.
XX 10-NOV-1997; 97US-00967113.
XX 22-SEP-1999; 99US-00401163.
XX 02-MAR-2001; 2001US-00798689.
XX
XX (ROCK/) ROCKWELL P.
XX (GOLD/) GOLDSTEIN N I.
XX
XX Rockwell P, Goldstein NI;
XX
XX WPI: 2003-801265/75.
XX P-PSDB; ADD24424.
XX
XX Inhibiting tumor growth by administering to a human a vascular
XX endothelial growth factor receptor (VEGFR) antagonist and epidermal
XX growth factor receptor (EGFR) antagonist.
XX
XX Example 12; SEQ ID NO 30; 90pp; English.
XX
XX The invention relates to a method of inhibiting tumour growth comprising
XX administering to a human a vascular endothelial growth factor receptor
XX (VEGFR) antagonist and epidermal growth factor receptor (EGFR)
XX antagonist. The method is useful for inhibiting tumour growth. The
XX present sequence is used in the exemplification of the invention.
XX
XX Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
XX
XX Query Match 67.3%; Score 238.4; DB 9; Length 348;
XX Best Local Similarity 82.3%; Pred. No. 1.5e-56;
XX Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
XX
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
Db 1 GAAGTGCAGCTGGTGGAGTCTGGGGCGGAGCCCTGGTCAAGCCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCCTGGCGACCTCCGGGTTCAAGTTCACTTCAATTAATCAATGACTGGTGGTCCGC 120
Db 61 TCCCTGGCGACCTCTG-----GATTCACCTTCAGTAGCTAGCATGAATGGTGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGCGGGCTGGAGTGGGTCTTCAACGATTAGTAGTGGTGGTATCCCA 180

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Db 115 CAGGCTCCAGGAAAGGGCTGGAGTGGGTCTCATTCATTAGTAGTAGTACTACATA 174
QY 181 TGGTACCCAGACTCCGTTGAAAGGGCAGATTCCATCTCCAGAGAGAACGCCCAACAACA 240
Db 175 TACTAACAGACTCAGTGAAGGCCCGATTCCATCTCCAGAGACCAACGCCCAAGGACTCA 234
QY 241 CTGTTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACACCGGCTCTTATTACTGTGGAGC 300
Db 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGGAGA 294
QY 301 TTGACTACAGGCTCTGACTCTGGGGCCAGGGAGTCTCTGGTCAACCCCTCTC 350
Db 295 GTACAGATGCTTTTGATATCTGGGGCCAAAGGACAAATGGTCAACCCCTCTC 344

RESULT 13
ID ADD80800 standard; DNA; 348 BP.
XX
XX ADD80800;
XX
XX 29-JAN-2004 (first entry)
XX Human clone D2H2 KDR-binding Fab variable heavy chain gene SEQ ID NO:30.
XX human; antibody; KDR; cytostatic; gene therapy; anti-KDR antibody;
XX tumour; angiogenesis; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..348
XX /*tag= a
XX /product= "KDR-binding Fab"
XX /note= "No start/stop codon given"
XX
XX WO2003075840-A2.
XX
XX 18-SEP-2003.
XX
XX 04-MAR-2003; 2003WO-US006459.
XX
XX 04-MAR-2002; 2002US-0361783P.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z;
XX
XX WPI: 2003-779032/73.
XX P-PSDB; ADD80801.
XX
XX New human anti-KDR antibody, useful for preparing a composition for
XX reducing tumor growth and inhibiting angiogenesis.
XX
XX Example 1; SEQ ID NO 30; 49pp; English.
XX
XX The invention relates to a novel isolated human antibody or its fragment
XX binds selectively to KDR. An antibody of the invention has cytostatic
XX activity, and may have a use in gene therapy. The antibody is anti-KDR
XX antibody. The antibody is useful for preparing a composition for reducing
XX tumour growth and inhibiting angiogenesis. The present sequence is used
XX in the exemplification of the invention.
XX
XX Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
XX
XX Query Match 67.3%; Score 238.4; DB 9; Length 348;
XX Best Local Similarity 82.3%; Pred. No. 1.5e-56;
XX Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
XX
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
Db 1 GAAGTGCAGCTGGTGGAGTCTGGGGCGGAGCCCTGGTCAAGCCCTGGGGGGTCCCTGAGACTC 60

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QY 61 TCCTGCGAGCCTCGGGTTTCAGGTTCACTTCAATAACTACTACATGGAGTGGGTCCGC 120
DB 61 TCCTGCGAGCCTCG-----GATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGC 114
QY 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGGATCCCA 180
DB 115 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTACATA 174
QY 181 TGGTAGCGAGACTCCGTGGAAGGCGAGATTCAACATCTCCAGAGAGAACGCCAAACACA 240
DB 175 TACTAGCGAGACTCAGTGAAGGCGCGATTCAACATCTCCAGAGAGAACGCCAAACACA 234
QY 241 CTTGTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGCGTGTCTATTACTGTGCGAGC 300
DB 235 CTGTATCTGCAATGAACAGCCTGAGAGCGCGAGGACACGCGTGTCTATTACTGTGCGAGA 294
QY 301 TTGACTACAGGCTGTGACTCTCGGGGCGAGGAGTCCCTGGTCAACGCTCTC 350
DB 295 GTCACAGATGCTTTTGATATCTGGGCGCAAGGAGCAATGGTCACCGTCTC 344

RESULT 14
AAS03478
ID AAS03478 standard; cDNA; 348 BP.
XX AC AAS03478;
XX 29-AUG-2001 (first entry)
DE DNA encoding anti-adipocyte monoclonal antibody heavy chain, FAT 65.
XX Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
KW heart disease; complementarity determining region; CDR; ss.
XX Homo sapiens.
XX WO200127279-A1.
XX 19-APR-2001.
XX 11-OCT-2000; 2000WO-GB003900.
XX 12-OCT-1999; 99US-0158812P.
XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Edwards BM, Main SH, Vaughan TJ;
PI WPI; 2001-282031/29.
DR P-PSDB; AAU02578.
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
PS Disclosure; Page 141; 182pp; English.

CC heart disease
XX Sequence 348 BP; 79 A; 91 C; 108 G; 70 T; 0 U; 0 Other;
SQ Query Match 67.1%; Score 237.4; DB 4; Length 348;
Best Local Similarity 82.2%; Pred. No. 2.9e-56; Indels 6; Gaps 1;
Matches 287; Conservative 0; Mismatches 56;
QY 2 AGGTGCGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCTGTGAGACTCT 61
DB 2 AGGTGCGAGCTGGTGGAGACCGGGGAGGCTTGGTCAAGCCTGGAGGGGCCCTGAGACTTT 61
QY 62 CCTCGGAGCCTCCGGGTTTCAGGTTCACTTCAATAACTACTACATGGAGTGGGTCCGCC 121
DB 62 CCTGTGAGCCTCTG-----GATTCACCTTCAGTAGCTACTACATGAGTGGATCCGCC 115
QY 122 AGGCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGGATCCCAAT 181
DB 116 AGGCTCCAGGCGAGGGCTGGAGTGGGTCTCATACATTAGTAGTAGTAGTATTACACAA 175
QY 182 GGTAGCGAGACTCCGTGGAAGGCGAGTTCACCATCTCCAGAGAGAACGCCAAACACAC 241
DB 176 ACTAGCGAGACTCTGTGAAGGGCGGATTCAACATTTCCAGAGACACGCCCAAGAACTCAC 235
QY 242 TGTTCCTTCAATGAACAGCCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTGCGAGCT 301
DB 236 TGTATCTGCAATGAACAGCCTGAGAGCGCGAGGACACGCGCTGTATTACTGTGCGAG 295
QY 302 TGACTACAGGCTGTGACTCTCTGGGGCGAGGAGTCTCTGTCCACGCTCTC 350
DB 296 ACGGAGGTGGTTCGACCCCTGGGGCGAGGCGACCCCTGGTCCACGCTCTC 344

RESULT 15
AAL43586
ID AAL43586 standard; DNA; 351 BP.
XX AC AAL43586;
XX 05-SEP-2002 (first entry)
DE Dig3 antibody heavy chain coding sequence.
XX 26-10 scFv antibody light chain; complementarity determining region 3;
KW CDR3; binding protein production; catalytic protein production; ds;
KW ligand structure determination; antibody isolation; dig3 heavy chain.
XX Unidentified.
XX Key Location/Qualifiers
FH 1..351
FT /*tag= a
FT /partial
FT /product= "Dig3 heavy chain"
FT /note= "No start or stop codon is given"
XX WO200234886-A2.
XX 02-MAY-2002.
XX 26-OCT-2001; 2001WO-US046795.
XX 27-OCT-2000; 2000US-00699023.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Chen G, Hayhurst A, Thomas JG, Iverson BL, Georgiou G;
XX WPI; 2002-500078/53.
XX P-PSDB; AAO15187.
XX Obtaining bacterium having nucleic acid encoding binding protein that
PT binds target ligand, or a nucleic acid encoding catalytic protein that

PT catalyzes reaction involving target substrate by display-less library
PT screening.
XX
XX Example 4; Page 97; 98pp; English.
XX
CC The invention comprises a method of obtaining a bacterium containing a
CC nucleic acid encoding a binding protein capable of binding a target
CC ligand, or a nucleic acid encoding a catalytic protein that catalyses a
CC reaction involving a target substrate. The method of the invention allows
CC the isolation of a cell expressing a nucleic acid encoding a binding
CC protein capable of binding a target ligand, and consequently the
CC isolation of the nucleic acid. The binding protein produced by the method
CC of the invention is useful in determining the structure of a target
CC ligand. The method of the invention is useful for the de novo isolation
CC of antibodies from large repertoire libraries and for monitoring
CC production during protein manufacturing. The method can also be used for
CC monitoring production of a particular byproduct of a biological reaction.
CC The present DNA sequence encodes the dig3 scFv antibody heavy chain which
CC is used in an example of the invention
XX
SQ Sequence 351 BP; 77 A; 85 C; 109 G; 80 T; 0 U; 0 Other;
Query Match 66.8%; Score 236.6; DB 6; Length 351;
Best Local Similarity 83.6%; Pred No. 4.9e-56;
Matches 295; Conservative 0; Mismatches 49; Indels 9; Gaps 2;
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGGCGAGCCTCCGGGTTTCAGGTTTCACTTCAATATCTACTAGTACTGGGTCCGC 120
DB 61 TCCTGGCGAGCCTCTG-----GATTCACCTTCAGTGACTACTATGAGCTGGATCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGCTATTAGTAGTGGTGTATCCACA 180
DB 115 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTGGTAGTACCATA 174
QY 181 TGGTAGCGAGACTCCGTGAGGGCAGATTTCACCTCTCCAGAGAGAGCCCAACACACA 240
DB 175 TACTACCGAGACTCTCTGAGGGCCGATTTCACCTCTCCAGGGAACGCCCAAGACTCA 234
QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGGAGC 300
DB 235 CTGTATCTCAATGAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGACA 294
QY 301 TTG---ACTACAGGCTGACTCTCTGGGGCCAGGGAGTCTGGTCAACCGTCTC 350
DB 295 ACGGGTTTTCCGGGGTTTGACTATTGGGGCCAGGTACCTTGGTCAACCGTCTC 347

Search completed: June 19, 2004, 08:21:28
Job time : 283 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 08:16:44 ; Search time 62 Seconds
(without alignments)
3168.591 Million cell updates/sec

Title: US-09-019-441A-7_COPY_58_411

Perfect score: 354

Sequence: 1 gaggtgagctgggtggagtc.....tccgtgcacgtctctca 354

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1059328

Minimum DB seq length: 0

Maximum DB seq length: 354

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	223.8	63.2	354	2	US-08-652-816A-21
2	223.2	63.1	354	2	US-08-652-816A-22
3	222.4	62.8	348	2	US-08-652-816A-24
4	215.4	60.8	351	2	US-08-428-197-35
5	215.4	60.8	351	5	PCT-US93-10555-35
6	214.2	60.5	345	2	US-08-428-197-41
7	214.2	60.5	345	5	PCT-US93-10555-41
8	213.6	60.3	294	2	US-08-428-197-47
9	213.6	60.3	294	5	PCT-US93-10555-47
10	212	59.9	354	2	US-08-958-201-1
11	206	56.5	354	2	US-08-958-201-3
12	196	55.4	348	2	US-09-184-658-10
13	196	55.4	348	4	US-09-504-262D-10
14	190	53.7	339	2	US-08-477-553A-52
15	187.8	53.1	351	3	US-09-240-274-184
16	186.8	52.8	285	3	US-09-043-514-1
17	186.8	52.8	306	2	US-08-273-146-64
18	185.4	52.4	354	4	US-09-530-139-21
19	183	51.7	351	4	US-09-339-922A-5
20	183	51.7	351	4	US-09-016-061-1
21	182.2	51.5	339	2	US-08-428-197-45
22	182.2	51.5	339	5	PCT-US93-10555-45
23	182.2	51.5	354	1	US-08-326-362-1
24	182.2	51.5	354	1	US-09-530-139-19
25	178.4	50.4	345	3	US-08-483-749A-5
26	178.4	50.4	351	4	US-09-339-922A-1
27	178.4	50.4	351	4	US-09-339-922A-1

28	178.4	50.4	351	4	US-08-791-391A-1
29	178.4	50.4	351	4	US-09-016-061-1
30	176.6	49.8	339	1	US-07-789-344A-9
31	176.2	49.3	335	2	US-08-477-553A-55
32	175.6	49.6	339	2	US-08-477-553A-54
33	175.4	48.4	342	2	US-08-477-553A-51
34	171.4	48.4	342	2	US-08-477-553A-53
35	169.2	47.8	342	2	PCT-US93-08435-9
36	168.2	47.5	354	5	US-09-530-139-17
37	167.8	47.4	342	4	US-09-042-353-139
38	165	46.6	297	4	US-08-758-417A-403
39	164.2	46.4	354	3	US-08-487-761-14
40	163.2	46.1	294	3	US-09-042-353-138
41	163.2	46.1	294	4	US-08-758-417A-402
42	162.4	45.9	318	1	US-08-129-930B-94
43	162.4	45.9	318	4	US-08-976-888A-94
44	161.4	45.6	294	3	US-09-042-353-132
45	161.4	45.6	294	3	US-09-042-353-136

ALIGNMENTS

RESULT 1
US-08-652-816A-21
; Sequence 21, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCaifferty, JG
; TITLE OF INVENTION: Specific binding members, materials and methods.
; NUMBER OF INVENTIONS: 53
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:

NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-816A-21

Query Match 63.2%; Score 223.8; DB 2; Length 354;
Best Local Similarity 80.8%; Pred. No. 2e-60;
Matches 290; Conservative 0; Mismatches 57; Indels 12; Gaps 2;

QY 2 AGGTGACGCTGTGAGCTCTGGGGGCGCTTGGCAAGCCTGGGGGGTCCCTGAGACTCT 61
DB 2 AGGTGACGCTGTGAGCTCTGGGGGCGCTTGGCAAGCCTGGGGGGTCCCTGAGACTCT 61

QY 62 CTTGGGCGAGCTCCGGGTTTCAGGTTTCACCTTCAATPACTACTACATGAGCTGGGTCCGCC 121
DB 62 CTTGGGCGAGCTCCGGGTTTCAGGTTTCACCTTCAATPACTACTACATGAGCTGGGTCCGCC 115

QY 122 AGGCTCCAGGCGAGGGCTGGAGTGGCTCTCAGTATTAGTAGTAGTGGTATCCCAT 181
DB 116 AGTCTCCAGGAGGAGCTGGAAATATGTTTCAGCTATTAGTAGTAAATGGGGGTAGCACT 175

QY 182 GGTACGACGACTCCGTGAAGGCGAGATTCAACCATCTCCAGAGAGAACCCCAACACAC 241
DB 176 ACTACGACGACTCCGTGAAGGCGAGATTCAACCATCTCCAGAGAGAACCCCAACACAC 235

QY 242 TGTTCCTTCAATGACAGCTCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGGAGCT 301
DB 236 TGTATCTTCAATGACAGCTCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGGAGCT 295

QY 302 TGA-----CTACAGGCTGCTACTCTCTGGGGCGAGGAGTCTGTGCTACCGTCTCTCA 354
DB 296 TTATAATCCCTACGGTATGAGAGCTCTGGGGCGAGGAGTCTGTGCTACCGTCTCTCA 354

RESULT 2

US-08-652-816A-22
Sequence 22, Application US/08652816A
Patent No. 5872215

GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-816A-22

Query Match 63.1%; Score 223.2; DB 2; Length 354;
Best Local Similarity 80.6%; Pred. No. 3e-60;
Matches 290; Conservative 0; Mismatches 58; Indels 12; Gaps 2;

QY 1 GAGTGCAGCTGTGAGTCTGGGGGCGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGTGCAGCTGTGAGTCTGGGGGCGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60

QY 61 TCCCTCCAGCCTCCGGGTTTCAGTTCACCTTCAATTAACCTACTACATGAGCTGGTCCGC 120
DB 61 TCCCTCCAGCCTCCGGGTTTCAGTTCACCTTCAATTAACCTACTACATGAGCTGGTCCGC 114

QY 121 CAGCTCCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTAGTAGTGTGTATCCACCA 180
DB 115 CAGCTCCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTAGTAGTGTGTATCCACCA 174

QY 181 TGGTACGAGCTCCGTGAGGCGAGATTCAACCATCTCCAGAGAGAACCCCAACACCA 240
DB 175 TACTACGAGACTCCGTGAGGCGAGATTCAACCATCTCCAGAGAGAACCCCAACACCA 234

QY 241 CTGTTTCTTCAATGAAACAGCTGAGAGCTGAGGACACCGCTGTCTATTACTGTGCGAG- 299
DB 235 CTGTTTCTTCAATGAAACAGCTGAGAGCTGAGGACACCGCTGTCTATTACTGTGCGAG- 294

QY 300 -----CTTGACTACAGGCTGTGACTCTCTGGGGCGAGGAGTCTGTGCTACCGTCTCTCA 354
DB 295 GCTTTGGTTCGGGAGTTATAAAGGACTGGGGCGAGGAGAACCCCTGGTCTCTCTCA 354

RESULT 3
US-08-652-816A-24
Sequence 24, Application US/08652816A
Patent No. 5872215

GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:

Qy 187 GCAGCTCCGTCGAGGCGAGTTCACCATCTCCAGAGAGAGCGCCAAACACACACTGTTT 246
Db 181 GCGGACTCCGTCGAGGCGCGGTTCACTCCATCTCCAGAGAGAGCGCCAAACACACTGTTT 240
Qy 247 CTTCAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTCTATTACTGTGCGAGCTTGAC- 305
Db 241 CTCGAATGAACAGCTGAGAGCGGAGAGACAGCGCTGTCTATTACTGTGCGAGAGATGCA 300
Qy 306 --TACAGGGTCTGACTCTCCGCGCCAGGGAGTCTGCTCACCGTCTCTCTCA 354
Db 301 TGGGATGCAATTCATATCTGGGCGCCAGGAGCAATGTCACAGTCTCTCTCA 351

RESULT 5

PCT-US93-10555-35
; Sequence 35, Application PC/TUS9310555
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Juba & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: SPA3-33
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..351
PCT-US93-10555-35

Query Match 60.8%; Score 215.4; DB 5; Length 351;
Best Local Similarity 80.1%; Pred. No. 8.2e-58;
Matches 281; Conservative 0; Mismatches 61; Indels 9; Gaps 2;

Qy 7 CAGCTGCTGAGTCTGGGCGCGCTTGGCAAGCTGGGGGCTCCCTGAGACTCTCTGTC 66
Db 7 CTGCTCGAGGAGTCTGGGCGCGCTTGGTACAGCTGGGGTCCCTGAGACTCTCTGTC 66
Qy 67 GCAGCTCCGCGGTTCAGGTTCACTTCACTACTACTAGGAGTGGTCCGCGAGCT 126
Db 67 GAAGCTCTG-----GATTCCCTTCAGTAACACTATGCGATGAGCTGGGTCGCGAGCT 120

Qy 127 CCAGGCGAGGCGCTGAGTGGGTCTCACTATTAGTAGTAGTGTGATCCCAACATGGTAC 186
Db 121 CCAGGCGAGGCGCTGAGTGGGTCTCACTATTAGTAGTAGTGTGATCCCAACATGGTAC 180
Qy 187 GCAGACTCCGTCGAGGCGAGTTCACCATCTCCAGAGAGAGCGCCAAACACACTGTTT 246
Db 181 GCGGACTCCGTCGAGGCGCGGTTCACTCCATCTCCAGAGAGAGCGCCAAACACTCTCTGTAT 240
Qy 247 CTTCAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTCTATTACTGTGCGAGCTTGAC- 305
Db 241 CTCGAATGAACAGCTGAGAGCGGAGAGACAGCGCTGTCTATTACTGTGCGAGAGATGCA 300
Qy 306 --TACAGGGTCTGACTCTCCGCGCCAGGGAGTCTGCTCACCGTCTCTCTCA 354
Db 301 TGGGATGCAATTCATATCTGGGCGCCAGGAGCAATGTCACAGTCTCTCTCA 351

RESULT 6

US-08-428-197-41
; Sequence 41, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Juba & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: SPAL-29
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..345
US-08-428-197-41

Query Match 60.5%; Score 214.2; DB 2; Length 345;
Best Local Similarity 79.6%; Pred. No. 1.9e-57;
Matches 281; Conservative 0; Mismatches 63; Indels 9; Gaps 2;

Qy 2 AGGTGACGTGCTGAGTCTGGGGGCGCGCTTGGCAAGCTGGGGGCTCCCTGAGACTCT 61


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Db 2 AGGTGAAGTCTCTGAGTCTGGGGGAGGCTTGGTACACCTGGGGGGTCCCTGAGACTCT 61
Qy 62 CTTGCGAGCTCCGGGTTCAAGTTCACTTCAATTAATCACTAATGAGACTGGGTCCGCC 121
Db 62 CTTGCGAGCTCCGGT-----GATTCACTTTAGTAATTATGCCATGAGCTGGGTCCGCC 115
Qy 122 AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGGTATTAGTAGTGGTATCCCAT 181
Db 116 AGGCTCCAGGGAGGGGCTGGAGTGGGTCTCAGGTATTAGTAGTGGTATCCCAT 175
Qy 182 GGTACGACAGCTCCGTGAAGGCGAGATTCACTATCCAGAGAGAACGCCAACACAC 241
Db 176 ACTACGACAGCTCCGTGAGGGGCGGTTCCCATCTCCAGAGAGAAATTTCAAGAACACGC 235
Qy 242 TGTTCCTCAATGAACAGCTGAGGCTGAGGACAGGCTGTCTATTACTGTGGAGCT 301
Db 236 TGTATCTCAATGAACAGCTGAGGCTGAGGACAGGCTGTGTATTACTGTGGTAGAG 295
Qy 302 TGACTACAGGGTCTGACTCCCTGGGGCCAGGGAGTCCCTGGTCAACCGTCTCTCA 354
Db 296 GATACAGCTACCGTG---TCTGGGGGCAAGGACCAAGGTCACCGTCTCTCTCA 345

RESULT 7
PCT-US93-10555-41
; Sequence 41, Application PC/TUS9310555
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: SpA1-29
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..345
PCT-US93-10555-41
Query Match 60.5%; Score 214.2; DB 5; Length 345;
Best Local Similarity 79.6%; Pred. No. 1.9e-57;
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Matches 281; Conservative 0; Mismatches 63; Indels 9; Gaps 2;
Qy 2 AGGTGAGCTGGTGGAGTCTGGGGGGGCTTGGCAAAGCTGGGGGGTCCCTGAGACTCT 61
Db 2 AGGTGAAGTCTCTGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGAGACTCT 61
Qy 62 CTTGCGAGCTCCGGGTTCAAGTTCACTTCAATTAATCACTAATGAGACTGGGTCCGCC 121
Db 62 CTTGCGAGCTCCGT-----GATTCACTTTAGTAATTATGCCATGAGCTGGGTCCGCC 115
Qy 122 AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGGTATTAGTAGTGGTATCCCAT 181
Db 116 AGGCTCCAGGGAGGGGCTGGAGTGGGTCTCAGGTATTAGTAGTGGTATCCCAT 175
Qy 182 GGTACGACAGCTCCGTGAAGGCGAGATTCACTATCCAGAGAGAACGCCAACACAC 241
Db 176 ACTACGACAGCTCCGTGAGGGGCGGTTCCCATCTCCAGAGAGAAATTTCAAGAACACGC 235
Qy 242 TGTTCCTCAATGAACAGCTGAGGCTGAGGACAGGCTGTCTATTACTGTGGAGCT 301
Db 236 TGTATCTCAATGAACAGCTGAGGCTGAGGACAGGCTGTGTATTACTGTGGTAGAG 295
Qy 302 TGACTACAGGGTCTGACTCCCTGGGGCCAGGGAGTCCCTGGTCAACCGTCTCTCA 354
Db 296 GATACAGCTACCGTG---TCTGGGGGCAAGGACCAAGGTCACCGTCTCTCTCA 345

RESULT 8
US-08-428-197-47
; Sequence 47, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: VH26C
```


Best Local Similarity 78.6%; Pred. No. 9.5e-57;
Matches 283; Conservative 0; Mismatches 65; Indels 12; Gaps 2;
QY 1 GAGGTGACAGCTGGTGGAGTCTGGGGGGGGCTGGCAAGGCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGACAGCTGGTGGAGTCTGGGGGGGGCTGGTACAGCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGGCAGCTCCGGGTTGAGTTCACTTCAATAACTACTACATGAGCTGGGTCGCG 120
Db 61 TCCTGGCAGCTCCGGT-----GAGTCACTTTAGCAGCCATGCCATGAGCTGGGTCGCG 114
QY 121 CAGGCTCCAGGGCAGGGCTGGAGTGGTCTCACTATTAGTAGTGGTGGATCCACACA 180
Db 115 CAGGCTCCAGGGAGGGCTGGAGTGGTCTCACTATTAGTAGTGGTGGATCCACACA 174
QY 181 TGGTACGACAGCTCCGGTGAAGGGGAGATTCACCATCTCCAGAGAGAACGCCAACACACA 240
Db 175 TACCGGACAGCTCCGGTGAAGGGGCGGTTCCATCTCCAGGGACAAATCCAAAGACAG 234
QY 241 CTGTTCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTGTGCGA-- 298
Db 235 GTGTATCTCAATGAACAGCTGCGAGCGGAGGACAGCGCCATATTACTGTGGGATT 294
QY 299 ----GCTTGACTACAGGTTGACTCTCGTGGGGCCAGGGAGTCTGGTCACTGCTCTCA 354
Db 295 TTAGGAGTAAATGGTTTGTATATCTGGGGCCAAAGGGACAATGGTCACTACTCTCA 354

RESULT 11

US-08-958-201-3
; Sequence 3, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; TITLE OF INVENTION: Specific binding members for estradiol;
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 1C
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..354
US-08-958-201-3

Query Match
Best Local Similarity 56.5%; Score 200; DB 2; Length 354;
Matches 283; Conservative 0; Mismatches 65; Indels 12; Gaps 2;

Matches 274; Conservative 0; Mismatches 74; Indels 12; Gaps 2;
QY 1 GAGGTGACAGCTGGTGGAGTCTGGGGGGGGCTGGCAAGGCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGACAGCTGGTGGAGTCTGGGGGGGGCTGGTACAGCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGGCAGCTCCGGGTTGAGTTCACTTCAATAACTACTACATGAGCTGGGTCGCG 120
Db 61 TCCTGGCAGCTCCGT-----GAGTCACTTTAGCAGCCATGCCATGAGCTGGGTCGCG 114
QY 121 CAGGCTCCAGGGCAGGGCTGGAGTGGTCTCACTATTAGTAGTGGTGGATCCACACA 180
Db 115 CAGGCTCCAGGGAGGGCTGGAGTGGTCTCACTATTAGTAGTGGTGGATCCACACA 174
QY 181 TGGTACGACAGCTCCGGTGAAGGGGAGATTCACCATCTCCAGAGAGAACGCCAACACACA 240
Db 175 NACCACGCGGACTCCGTGAAGGGGCGGTTCCATCTCCAGGGACAAATTCAGAGACAG 234
QY 241 CTGTTCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTGTGCGA-- 298
Db 235 GTGTATCTCAATGAACAGCTGCGAGCGGAGGACAGCGCCATATTACTGTGGGATT 294
QY 299 ----GCTTGACTACAGGTTGACTCTCGTGGGGCCAGGGAGTCTGGTCACTGCTCTCA 354
Db 295 TTAGGAGTAAATGGTTTGTATATCTGGGGCCAAAGGGACAATGGTCACTACTCTCA 354

RESULT 12

US-09-184-658-10
; Sequence 10, Application US/09184658
; Patent No. 6030792
; GENERAL INFORMATION:
; APPLICANT: Otterness, Ivan G.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Downs, James T.
; APPLICANT: Johnson, Kimberly S.
; TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
; FILE REFERENCE: PC9946-A
; CURRENT APPLICATION NUMBER: US/09/184,658
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/065,423
; EARLIER FILING DATE: 1997-11-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: V region
; LOCATION: (1)..(348)
; OTHER INFORMATION: Mature 5109 VH region.
US-09-184-658-10

Query Match
Best Local Similarity 55.4%; Score 196; DB 3; Length 348;
Matches 263; Conservative 0; Mismatches 85; Indels 6; Gaps 1;

QY 1 GAGGTGACAGCTGGTGGAGTCTGGGGGGGGCTGGCAAGGCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGACAGCTGGTGGAGTCTGGGGGGGGCTGGTACAGCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGGCAGCTCCGGGTTGAGTTCACTTCAATAACTACTACATGAGCTGGGTCGCG 120
Db 61 TCCTGGCAGCTCCGT-----GATTCACTTTCAATACCTACGGCATGTCTTGGGTTGCG 114
QY 121 CAGGCTCCAGGGCAGGGCTGGAGTGGTCTCACCTATTAGTAGTGGTGGATCCACACA 180
Db 115 CAGACTCCAGACAGAGAGCTGGAGTGGTGGCAACCATATTATAGTGTGTCTCACC 174
QY 181 TGGTACGACAGCTCCGTGAAGGGGAGATTCACCATCTCCAGAGAGAACGCCAACACACA 240

Db 175 TTTTATGACAGAGTGTGAAGGGCGGATTACCAATTTCCAGAGACATGCCAAAACACC 234
Qy 241 CTGTTTCTTCAAAATGAACAGAGCTGAGAGTGAAGACAGCGGTGCTATTAATCTGTGGAGC 300
Db 235 CTGTATCTGCAATCAACAGAGCTGAAGTCTGGGAGCTCAGCATATTAATCTGTGAAGA 294
Qy 301 TTGACTACAGGCTGACTCTCTGGGGCCAGGAGTCTGTGGTCAACCGTCTCTCA 354
Db 295 GGATATAGTAATACCTCGCTGGGGCCAAAGGGCGCTGGTCACTGTCTGTGCA 348

RESULT 13
US-09-504-262D-10
; Sequence 10, Application US/09504262D
; Patent No. 6642007
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Saltarelli, Mary J.
; APPLICANT: Johnson, Kimberly S.
; APPLICANT: Otterness, Ivan G.
; TITLE OF INVENTION: Assays for Measurement of Type II Collagen Fragments in Urine
; FILE REFERENCE: PCI0189GR - CIP of PC9946A
; CURRENT APPLICATION NUMBER: US/09/504,262D
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-504-262D-10

Query Match 55.4%; Score 196; DB 4; Length 348;
Best Local Similarity 74.3%; Pred. No. 9.3e-52;
Matches 263; Conservative 0; Mismatches 85; Indels 6; Gaps 1;
Qy 1 GAGGTGACAGGCTGAGTGTCTGGGGCGGCTGGCAAGAGCTGGGGGTCCCTCAGACTC 60
Db 1 GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTCAGTGCAGGCTGGAGGTCCCTGAAACTC 60
Qy 61 TCTCGCAGAGCTCCGGGTTCAGGTTTACCTTTCAATAACTACTACATGAGTGGTCCGC 120
Db 61 TCTGTGAGAGCTCTG-----GATTCATTCATATACCTAGCGCATGTCTGGGTTCGC 114
Qy 121 CAGGTTCAGAGGCGAGGCTGAGTGGGTCTCACTATTAATAGTGTGGTGTATCCACA 180
Db 115 CAGACTCCAGACAGAGGCTGGAGTGGGTGGCAACCTTAATAGTGTGGTGTCTCACC 174
Qy 181 TGGTACGACAGCTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db 175 TTATATGACAGAGTGTGAGGCGCGATTCACCAATTCAGAGACATATGCCAAAACACC 234
Qy 241 CTGTTTCTTCAATGAACAGCTGAGAGTGTGAGGACAGCGCTGTCTATTACTGTGGAGC 300
Db 235 CTGTATCTGCAATGAACAGGCTGAAGTCTGGGGAGCTCAGGCAATGATTAATCTGTGAAGA 294
Qy 301 TTGACTACAGGCTGACTCTCTGGGGCCAGGAGTCTGGTCAACCGTCTCTCTCA 354
Db 295 GGATATAGTAATACCTCGCTGGGGCCAAAGGGCGCTGGTCACTGTCTGTGCA 348

RESULT 14
US-08-477-553A-52
; Sequence 52, Application US/08477553A
; Patent No. 5919910
; GENERAL INFORMATION:
; APPLICANT: HUGHES-JONES, Nevin C
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria

STATE: VA
COUNTRY: USA
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,553A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,034
FILING DATE: 23-JUNE-1992
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8925590.5
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 007330-032
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..339
OTHER INFORMATION: /note= "Nucleotides 1-378 corres.
to nucleotides 24-362 of Fig. 11/14. Nucleotides
1-23 and 363-378 represent PCR primers."
US-08-477-553A-52

Query Match 53.7%; Score 190; DB 2; Length 339;
Best Local Similarity 83.3%; Pred. No. 6.9e-50;
Matches 230; Conservative 0; Mismatches 40; Indels 6; Gaps 1;
Qy 24 GGGGGCTTCGCAAGAGCTGGGGGGTCCCTGAGACTCTCTCGCGCAGCCTCCGGGTTTCA 83
Db 1 GGGAGGCTTATTTAGCTGGGGGGTCCCTGAGACTCTCTCTGCGAGCTCTGA----- 55
Qy 84 GTTCACCTTCAATAACTTACTACATGAGTGGGTCCGCGCAGGCTCCAGGCGAGGGGCTTGA 143
Db 56 -TTCACTTCAGTAGTTACTGATGCACTGGGTCCGCGCAAGCTCCAGGGAGGGGCTTGT 114
Qy 144 GTGGCTCTCAGTATTAGTAGTGTGATCCACATGCTACGACACTCCGTTGAAGGG 203
Db 115 GTGGGTCTCAGTATTATTAATAGTTATGATAGTATGACCAAGTTAGCGAGTCCGTTGAAGGG 174
Qy 204 CAGATTACCATCTCCAGAGAGAACGCCAACACACTGTCTTCTTCAATGAACAGCT 263
Db 175 CCGATTACCATCTCCAGAGAGAACGCCAACACACTGTCTTCTGCAAAATGAACACTCT 234
Qy 264 GAGAGCTGAGGACAGCGGCTCTTATTACTGTGGAG 299
Db 235 GAGAGCGGAGGACAGCGCTGTGTATTACTGTGCAAG 270

RESULT 15
US-09-240-274-184
; Sequence 184, Application US/09240274
; Patent No. 625455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rb(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

Mon Jun 21 11:45:43 2004

;; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

;; FILE REFERENCE: 09596-42U2

;; CURRENT APPLICATION NUMBER: US/09/240,274

;; EARLIER FILING DATE: 1999-01-29

;; EARLIER APPLICATION NUMBER: 60/081,380

;; EARLIER FILING DATE: 1998-04-10

;; EARLIER APPLICATION NUMBER: 60/028,550

;; EARLIER FILING DATE: 1996-10-11

;; NUMBER OF SEQ ID NOS: 224

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 184

;; LENGTH: 351

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE: OTHER INFORMATION: anti-Rh(D) antibody clone SH17

;; FEATURE: OTHER INFORMATION: anti-Rh(D) antibody clone SH17

;; OTHER INFORMATION: anti-Rh(D) antibody clone SH17

;; US-09-240-274-184

Query Match 53.1%; Score 187.8; DB 3; Length 351;

Best Local Similarity 74.5%; Pred. No. 3.4e-49;

Matches 266; Conservative 0; Mismatches 82; Indels 9; Gaps 2;

QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 60

DB 1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCCGGGGGTCCCTGAGACTC 60

QY 61 TCCTGGCGCAGCCTCCGGGTTCAAGTTTCACTTCAATAACTACTATCATGGACTGGGTCCGC 120

DB 61 TCCTGGGTGGCTCTG-----GAATCCCTTTGTTTCTCTTGGATGGCTGGGTCCGC 114

QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGTCTCAGGTATTAGTAGTAGTGTGATCCACACA 180

DB 115 CAGGCCCCAGGGAAGGGGCTGGAGTGGGTGGCCAAACATAAACAGATGGAAGTAAGAAA 174

QY 181 TGGTAGCGAGACTCCGTGAAGGGCAGATTCAACATCTCCAGAGAGAAAGCCCAACACACA 240

DB 175 AACTATGTGACTCTCTGTGGAGGCCGATTCAACATCTCCAGAGACAAACGGAAGAACTCA 234

QY 241 CTGTTTCTTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGGAG- 299

DB 235 CTTTATCTGCAATGACAGCCTGAGAGCCGAGGACACGCGGATATATTACTGTGGCGGA 294

QY 300 --CTTGACTACAGGCTCTGACTCTCGGGCCAGGGAGTCTGTGTACCGTCTCCTCA 354

DB 295 GATTCACTTACTTGTGTTTGTACTCTGGGCCAGGAGCCCTGGTCAACCGTCTCCTCA 351

Search completed: June 19, 2004, 09:58:55

Job time : 64 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 08:52:24 ; Search time 285 Seconds
(without alignments)
5890.195 Million cell updates/sec

Title: US-09-019-441a-7_COPY_58_411

Perfect score: 354

Sequence: 1 gagggtgcagctggggagtc.....tccgtgcacgcgtctctca 354

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 2593982

Minimum DB seq length: 0

Maximum DB seq length: 354

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/prodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/prodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq.*
- 17: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq.*
- 18: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	241.6	68.2	348	15	US-10-091-300-23
2	240	67.8	348	15	Sequence 23, Appl
3	238.4	67.3	348	15	Sequence 27, Appl
4	232.6	65.7	351	17	US-10-091-300-30
5	223.8	63.2	349	12	US-10-466-836-25
6	223.8	63.2	349	12	Sequence 25, Appl
7	222.6	62.9	294	16	US-10-269-711-18
8	222.6	62.9	311	9	Sequence 18, Appl
9	221.6	62.6	296	17	US-10-269-711-38
10	219.4	62.0	294	16	Sequence 17, Appl
11	219	61.9	348	15	Sequence 3233, A
12	218.4	61.7	345	15	Sequence 29, Appl
13	218.2	61.6	351	13	Sequence 20, Appl
14	216.8	61.2	296	13	Sequence 15, Appl
					Sequence 11, Appl
					Sequence 23, Appl
					Sequence 1, Appl

15	216.8	61.2	296	17	US-10-038-591-31	Sequence 31, Appl
16	215.8	61.0	354	15	US-10-120-377-74	Sequence 74, Appl
17	214.4	60.6	345	17	US-10-408-901-17	Sequence 17, Appl
18	211.4	59.7	291	16	US-10-251-215-18	Sequence 18, Appl
19	211.4	59.7	327	15	US-10-029-386-24519	Sequence 24519, A
20	208.4	59.2	348	17	US-10-408-901-13	Sequence 13, Appl
21	208.8	59.0	302	17	US-10-432-409A-175	Sequence 175, Appl
22	207.8	58.7	354	15	US-10-324-493-7	Sequence 7, Appl
23	205.6	58.1	348	16	US-10-338-366-1	Sequence 1, Appl
24	205	57.9	291	16	US-10-251-215-21	Sequence 21, Appl
25	204	57.6	302	17	US-10-432-409A-170	Sequence 170, Appl
26	203.6	57.5	345	9	US-09-974-449-1	Sequence 1, Appl
27	202.8	57.3	342	13	US-10-147-849-4	Sequence 4, Appl
28	200.8	56.7	354	16	US-10-173-551-13	Sequence 13, Appl
29	200	56.5	345	17	US-10-408-901-9	Sequence 9, Appl
30	198.2	56.0	348	17	US-10-408-901-21	Sequence 21, Appl
31	197.6	55.8	294	13	US-09-948-939-14	Sequence 14, Appl
32	197.6	55.8	296	13	US-09-948-939-20	Sequence 20, Appl
33	197.6	55.8	296	15	US-10-320-094-12	Sequence 12, Appl
34	197.6	55.8	329	15	US-10-010-729-34	Sequence 34, Appl
35	195.4	55.2	294	10	US-09-995-529-7	Sequence 7, Appl
36	195.4	55.2	294	13	US-09-948-939-2	Sequence 2, Appl
37	195.2	55.1	349	12	US-10-408-901-5	Sequence 5, Appl
38	193.8	54.7	348	17	US-10-338-366-51	Sequence 51, Appl
39	193.8	54.7	294	16	US-10-408-901-25	Sequence 25, Appl
40	193.4	54.6	348	17	US-10-408-901-25	Sequence 25539, A
41	192.2	54.3	303	9	US-09-864-761-22022	Sequence 22022, A
42	192.2	54.3	308	15	US-10-029-386-25539	Sequence 25539, A
43	191	54.0	288	16	US-10-251-215-19	Sequence 19, Appl
44	189.2	53.4	351	13	US-10-357-864A-55	Sequence 55, Appl
45	189.2	53.4	351	17	US-10-399-518-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1

US-10-091-300-23
; Sequence 23, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; TITLE OF INVENTION: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
; FILE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091,300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-23

Query Match 68.2%; Score 241.6; DB 15; Length 348;
Best Local Similarity 82.9%; Pred. No. 1.8e-66;
Matches 290; Conservative 0; Mismatches 54; Indels 6; Gaps 1;

QY	1	GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC	60
DB	1	GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC	60
QY	61	TCCTGCGCAGCTCCGGGTTACAGTTTCACCTTCAATAACTACTATACATGAGCTGGGTCCGC	120
DB	61	TCCTGCGCAGCTCCGGTGGTTCACCTTCAATAACTACTATACATGAGCTGGGTCCGC	114
QY	121	CAGGCTCCAGGCGGAGGCTGGAGTGGGTCTCCACCTATTAGTAGTGTGTATCCACA	180
DB	115	CAGGCTCCAGGCGGAGGCTGGAGTGGGTCTCCACCTATTAGTAGTGTGTATCCACA	174
QY	181	TGTAAGCAGACTCCGTGAAGGCGGAGTTCACCATCTCCAGAGAGAACCCCAACACA	240

Db 175 TACTACGAGACTCAGTGAAGGCGGATTTCACCATCTCCAGAGACACGCCAAGAACTCA 234
Qy 241 CTGTTCTTCAATGAACAGCCTCAGAGCTGAGGACAGGCTCTCTATTACTGTGGAGC 300
Db 235 CTGATCTGCAATGAACAGCCTCAGAGCGGAGGACACGCTGTGTATTACTGTGGAGA 294
Qy 301 TTGACTACAGGCTCTGACTCTCGGGGCGAGGAGTCTCTGGTCAACCGTCTC 350
Db 295 GTCACAGATGCTTTTGATATCTGGGCGCAAGGACAAATGTCACCGTCTC 344

RESULT 2

US-10-091-300-27
; Sequence 27, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-27

Query Match 67.8%; Score 240; DB 15; Length 348;
Best Local Similarity 82.6%; Pred. No. 5.8e-66;
Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;

Qy 1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCTCGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCTCGGGGGTCCCTGAGACTC 60
Qy 61 TCCTGCGCAGCTCCGGGTTTCAGGTTTCACTTCAATAACTACTATACATGAGACTGGGTCCGC 120
Db 61 TCCTGCGCAGCTCCGGGTTTCAGGTTTCACTTCAATAACTACTATACATGAGACTGGGTCCGC 114
Qy 121 CAGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATTAGTAGTAGTGGTATCCACA 180
Db 115 CAGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATTAGTAGTAGTGGTATCCACA 174
Qy 181 TGSTACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACCCCAACACACA 240
Db 175 TACTACGAGACTCAGTGAAGGCGGATTCCACCATCTCCAGAGAGAACCCCAAGAACTCA 234
Qy 241 CTGTTCTTCAATGAACAGCCTCAGAGCTGAGGACAGCGCTCTTATTACTGTGGAGC 300
Db 235 CTGATCTGCAATGAACAGCCTCAGAGCGGAGGACACGCTGTGTATTACTGTGGAGA 294
Qy 301 TTGACTACAGGCTCTGACTCTCGGGCGAGGAGTCTCTGGTCAACCGTCTC 350
Db 295 GTCACAGATGCTTTTGATATCTGGGCGCAAGGACAAATGTCACCGTCTC 344

RESULT 3

US-10-091-300-30
; Sequence 30, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT FILING DATE: 2002-03-04

; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 30
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-30

Query Match 67.3%; Score 238.4; DB 15; Length 348;
Best Local Similarity 82.3%; Pred. No. 1.9e-65;
Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;

Qy 1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCTCGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCTCGGGGGTCCCTGAGACTC 60
Qy 61 TCCTGCGCAGCTCCGGGTTTCAGGTTTCACTTCAATAACTACTATACATGAGACTGGGTCCGC 120
Db 61 TCCTGCGCAGCTCCGGGTTTCAGGTTTCACTTCAATAACTACTATACATGAGACTGGGTCCGC 114
Qy 121 CAGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATTAGTAGTAGTGGTATCCACA 180
Db 115 CAGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATTAGTAGTAGTGGTATCCACA 174
Qy 181 TGSTACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACCCCAACACACA 240
Db 175 TACTACGAGACTCAGTGAAGGCGGATTCCACCATCTCCAGAGAGAACCCCAAGAACTCA 234
Qy 241 CTGTTCTTCAATGAACAGCCTCAGAGCTGAGGACAGCGCTCTTATTACTGTGGAGC 300
Db 235 CTGATCTGCAATGAACAGCCTCAGAGCGGAGGACACGCTGTGTATTACTGTGGAGA 294
Qy 301 TTGACTACAGGCTCTGACTCTCGGGCGAGGAGTCTCTGGTCAACCGTCTC 350
Db 295 GTCACAGATGCTTTTGATATCTGGGCGCAAGGACAAATGTCACCGTCTC 344

RESULT 4

US-10-466-836-25
; Sequence 25, Application US/10466836
; Publication No. US20040110922A1
; GENERAL INFORMATION:
; APPLICANT: GAVISH-GALILIE BIO-APPLICATIONS LTD.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR PREVENTION AND TREATMENT OF HIV
; FILE REFERENCE: GAVISH-003 PCT
; CURRENT APPLICATION NUMBER: US/10/466,836
; CURRENT FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 25
; LENGTH: 351
; TYPE: DNA
; ORGANISM: HUMAN
US-10-466-836-25

Query Match 65.7%; Score 232.6; DB 17; Length 351;
Best Local Similarity 82.4%; Pred. No. 1.3e-63;
Matches 294; Conservative 0; Mismatches 54; Indels 9; Gaps 2;

Qy 1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCTCGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGGTACAGCTCGGGGGTCCCTGAGACTC 60
Qy 61 TCCTGCGCAGCTCCGGGTTTCAGGTTTCACTTCAATAACTACTATACATGAGACTGGGTCCGC 120
Db 61 TCCTGCGCAGCTCCGGGTTTCAGGTTTCACTTCAATAACTACTATACATGAGACTGGGTCCGC 114
Qy 121 CAGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATTAGTAGTAGTGGTATCCACA 180
Db 115 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATTAGTAGTAGTGGTATCCACA 174

QY 181 TGGTACGAGACTCGTGAAGGCGGAGTTCACCATCTCCAGAGAGAGCGCAACACACA 240
DB 173 TACTACGAGAGCTCGTGAAGGCGGCTTCACCATCTCCAGAGAGAGCGCAACACAG 234
QY 241 CTGTTCTTCAAAATGAACAGAGCTGAGAGCTGAGAGACAGGCTGTCTATTACTGTGCA-- 298
DB 235 CTGTATCTGCAAAATGAACAGAGCTGAGAGCTGAGAGACAGGCGGCTGTATTACTGTGCA 294
QY 299 -GCTTGACTACAGGCTGTGACTCTCGGGGCGAGAGGCTCTGTGTCACCGTCTCTCA 354
DB 295 CGGGGCGATCGTGCTTTTGACTATTGGGGGCGAAGGTACCGTGTGTCACCGTCTCTCA 351

RESULT 5

US-10-269-711-18
; Sequence 18, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989.US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-711-18

Query Match 63.2%; Score 223.8; DB 12; Length 349;
Best Local Similarity 79.3%; Pred. No. 8.1e-61;
Matches 280; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

QY 2 AGGTGCAAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCGCTGGGGGCTCCCTGAGACTCT 61
DB 2 AGGTGCAAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCGCTGGGGGCTCCCTGAGACTCT 61
QY 62 CCTGCGAGCTCGTGGAGTCTGGGGGCGGCTTGGCAAGCGCTGGGGGCTCCCTGAGACTCT 121
DB 62 CCTGCGAGCTCGTGGAGTCTGGGGGCGGCTTGGCAAGCGCTGGGGGCTCCCTGAGACTCT 115
QY 122 AGGTCCAGGCGAGGCGCTGGAGTGGGTCTCACTATTACTACTACTACTACTACTACTACT 181
DB 116 AGGTCCAGGCGAGGCGCTGGAGTGGGTCTCACTATTACTACTACTACTACTACTACTACT 175
QY 182 GGTACGAGACTCGTGAAGGCGAGATTCACCATCTCCAGAGAGAGCGCAACACACAC 241
DB 176 ACTATGAGACTCGTGAAGGCGAGATTCACCATCTCCAGAGAGAGCGCAACACACACCG 235
QY 242 TGTTTCTTCAAAATGAACAGCTGAGAGCTGAGAGACAGGCTGTCTATTACTGTGCGAGCT 301
DB 236 TGTATCTGCAAAATGAACAGCTGAGAGCTGAGAGACAGGCTGTCTATTACTGTGCGAGAG 295
QY 302 TGACTACAGGCTCTGACTCTGGGGGCGAGGAGTCTGTGTCACCGTCTCTCA 354
DB 296 GTCCGTACTACTTGTACTACTGGGGGCGAGGAGCGCTGTGTCACCGTCTCTCA 348

RESULT 6

US-10-269-711-38
; Sequence 38, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.

; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989.US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-711-38

Query Match 63.2%; Score 223.8; DB 12; Length 349;
Best Local Similarity 79.3%; Pred. No. 8.1e-61;
Matches 280; Conservative 0; Mismatches 57; Indels 6; Gaps 1;
QY 2 AGGTGCAAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCGCTGGGGGCTCCCTGAGACTCT 61
DB 2 AGGTGCAAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCGCTGGGGGCTCCCTGAGACTCT 61
QY 62 CCTGCGAGCTCGTGGAGTCTGGGGGCGGCTTGGCAAGCGCTGGGGGCTCCCTGAGACTCT 121
DB 62 CCTGCGAGCTCGTGGAGTCTGGGGGCGGCTTGGCAAGCGCTGGGGGCTCCCTGAGACTCT 115
QY 122 AGGTCCAGGCGAGGCGCTGGAGTGGGTCTCACTATTACTACTACTACTACTACTACTACT 181
DB 116 AGGTCCAGGCGAGGCGCTGGAGTGGGTCTCACTATTACTACTACTACTACTACTACTACT 175
QY 182 GGTACGAGACTCGTGAAGGCGAGATTCACCATCTCCAGAGAGAGCGCAACACACAC 241
DB 176 TCTATGAGACTCGTGAAGGCGAGATTCACCATCTCCAGAGAGAGCGCAACACACACCG 235
QY 242 TGTTTCTTCAAAATGAACAGCTGAGAGCTGAGAGACAGGCTGTCTATTACTGTGCGAGCT 301
DB 236 TGTATCTGCAAAATGAACAGCTGAGAGCTGAGAGACAGGCTGTCTATTACTGTGCGAGAG 295
QY 302 TGACTACAGGCTCTGACTCTGGGGGCGAGGAGTCTGTGTCACCGTCTCTCA 354
DB 296 GCGGGAGCTACTGGGAGCTACTGGGGGCGAGGAGCGCTGTGTCACCGTCTCTCA 348

RESULT 7

US-10-251-215-17
; Sequence 17, Application US/10251215
; Publication No. US20030219839A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Frederickson, Shana
; TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 1087-36
; CURRENT APPLICATION NUMBER: US/10/251,215
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/323,537
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/323,544
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/379,980
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 294
; TYPE: DNA
; ORGANISM: human
US-10-251-215-17

Query Match 62.9%; Score 222.6; DB 16; Length 294;
 Best Local Similarity 86.6%; Pred. No. 1.9e-60;
 Matches 259; Conservative 0; Mismatches 34; Indels 6; Gaps 1;
 1 GAGGTCCAGCTGTGGAGTCTGGGGCGCTTGGCAAGCCCTGGGGGTCTCTGAGACTC 60
 1 GAGGTCCAGCTGTGGAGTCTGGGGCGCTTGGCAAGCCCTGGGGGTCTCTGAGACTC 60
 61 TCTGCGCAGCTTCCCGGCTCAGGTTCACTTCAATTAATCTACATGACTGGGTCCGC 120
 61 TCTGTCGAGCTCTG-----GATTCACCTTCAGTAGTATAGATGAATGGTCCGC 114
 121 CAGGCTCCAGGCGAGGGCTGAGTGGTCTCAGCTATAGTAGTAGTGGTATCCACACA 180
 115 CAGGCTCCAGGCGAGGGCTGAGTGGTCTCAGCTATAGTAGTAGTGGTATCCACACA 174
 181 TGTAGCCAGACTCCCGTGAAGGCGAGATTCACCATCTCCAGAGAGAGCCCAACACACA 240
 175 TACTAGCAGACTCAGTGAAGGCGGATTCACCATCTCCAGAGAGAGCCCAACACTCA 234
 241 CTGTTCTTCAATGAAGCTGAGCTGAGGACAGGCTGTCTATTACTGTGGGAG 299
 235 CTGTATCTCAATGAAGCTGAGCTGAGGACAGGCTGTCTATTACTGTGGGAG 293

RESULT 8
 US-09-864-761-31233
 ; Sequence 31233, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aemica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/130,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/532,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,587
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/508,409
 ; PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
 SEQ ID NO 31233
 LENGTH: 311
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AB019439.1
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.51
 OTHER INFORMATION: EST HUMAN HIT: AW403220.1, EVALUATE 0.00e+00
 OTHER INFORMATION: NT HIT: L29155.1, EVALUATE 0.00e+00
 OTHER INFORMATION: SWISSPROT HIT: P01764, EVALUATE 3.00e-43
 US-09-864-761-31233
 Query Match 62.9%; Score 222.6; DB 9; Length 311;
 Best Local Similarity 86.6%; Pred. No. 1.9e-60;
 Matches 259; Conservative 0; Mismatches 34; Indels 6; Gaps 1;
 1 GAGGTCCAGCTGTGGAGTCTGGGGCGCTTGGCAAGCCCTGGGGGTCTCTGAGACTC 60
 12 GAGGTCCAGCTGTGGAGTCTGGGGCGCTTGGCAAGCCCTGGGGGTCTCTGAGACTC 71
 61 TCTGCGCAGCTTCCCGGCTCAGGTTCACTTCAATTAATCTACATGACTGGGTCCGC 120
 72 TCTGTCGAGCTCTG-----GATTCACCTTCAGTAGTATAGATGAATGGTCCGC 125
 121 CAGGCTCCAGGCGAGGGCTGAGTGGTCTCAGCTATAGTAGTAGTGGTATCCACACA 180
 126 CAGGCTCCAGGCGAGGGCTGAGTGGTCTCAGCTATAGTAGTAGTGGTATCCACACA 185
 181 TGTAGCCAGACTCCCGTGAAGGCGAGATTCACCATCTCCAGAGAGAGCCCAACACACA 240
 186 TACTAGCAGACTCAGTGAAGGCGGATTCACCATCTCCAGAGAGAGCCCAACACTCA 245
 241 CTGTTCTTCAATGAAGCTGAGCTGAGGACAGGCTGTCTATTACTGTGGGAG 299
 246 CTGTATCTCAATGAAGCTGAGCTGAGGACAGGCTGTCTATTACTGTGGGAG 304

RESULT 9
 US-10-038-591-29
 ; Sequence 29, Application US/10038591
 ; Publication No. US20040086503A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Bruce D.
 ; APPLICANT: Beebe, Jean
 ; APPLICANT: Miller, Penelope E.
 ; APPLICANT: Moyer, James D.
 ; APPLICANT: Corvalan, Jose R.
 ; APPLICANT: Gallo, Michael
 ; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
 ; FILE REFERENCE: ABX-PF2
 ; CURRENT APPLICATION NUMBER: US/10/038,591
 ; CURRENT FILING DATE: 2002-01-04
 ; PRIOR APPLICATION NUMBER: 60/259,927
 ; PRIOR FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 29
 ; LENGTH: 296
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-038-591-29
 Query Match 62.6%; Score 221.6; DB 17; Length 296;
 Best Local Similarity 86.6%; Pred. No. 3.9e-60;
 Matches 258; Conservative 0; Mismatches 34; Indels 6; Gaps 1;
 2 AGGTCCAGCTGTGGAGTCTGGGGCGCTTGGCAAGCCCTGGGGGTCTCTGAGACTCT 61

```

Db      2 AGGTGAGCTGTGGTGGAGTCTGGGGGAGGCTGTGGTCAAGCCCTGGAGGGTCCCTGAGACTCT 61
Qy      62 CTTGCGAGCTCCGGGTTCAGGTTCACTTCAATACTACTCATGACTGGTGGTCCGCC 121
Db      62 CTTGCGAGCTCTG-----GATTCACTTTCAGTGACTACTCATGACTGGATCCGCC 115
Qy      122 AGGTCCAGGCGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTATCCCAT 181
Db      116 AGGTCCAGGAGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTATCCCAT 175
Qy      182 GGTACGGAGCTCCGTGAAGGCGAGATTCACATCTCCAGAGAAAGCCCAACACAC 241
Db      176 ACTACGAGACTCTGTGAAGGCGGATTTCACATCTCCAGGAGCAAGCCCAAGAACTCAC 235
Qy      242 TGTTCCTTCAATGAACAGCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTCCGAG 299
Db      236 TGTATCTCAATGAACAGCTGAGAGCGGAGGAGGAGGCGGCGTGTATTACTGTCCGAG 293

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RESULT 10
US-10-251-215-20
; Sequence 20, Application US/10251215
; Publication No. US20030219839A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED
; TITLE OF INVENTION: ANTI-PDGF ANTIBODIES
; FILE REFERENCE: 1087-36
; CURRENT APPLICATION NUMBER: US/10/251,215
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/323,537
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/323,544
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/379,980
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 20
; LENGTH: 294
; TYPE: DNA
; ORGANISM: human
US-10-251-215-20

```

```

Query Match      62.0%; Score 219.4; DB 16; Length 294;
Best Local Similarity 86.0%; Pred. No. 1.9e-59;
Matches 257; Conservative 0; Mismatches 36; Indels 6; Gaps 1;

Qy      1 GAGGTGCGAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTC 60
Db      1 GAGGTGCGAACTGGTGGAGTCTGGGGGAGGCTGGTCAAGCTTGGGGGTCCCTGAGACTC 60
Qy      61 TCCTGCGAGCTCCGGGTTCAGGTTCACCTTCAATAA CTACTACATGAGTGGGTCCGC 120
Db      61 TCCTGTCCAGCTCTG-----GATTCACTTTCAGTAGCTATAGCATCAACTGGGTCCGC 114
Qy      121 CAGGTCCAGGCGAGGCTGGAGTGGGCTTCACTTCACTATTAGTAGTGGTATCCCA 180
Db      115 CAGGTCCAGGAGAGGGCTGGAGTGGGCTTCACTTCACTATTAGTAGTGGTATCCCA 174
Qy      181 TGGTACGAGACTCCGTGAAGGCGAGATTCACATCTCCAGAGAAAGCCCAACACAC 240
Db      175 TACTACGAGACTCACTGAAGGCGGATTCACATCTCCAGAGAAAGCCCAAGAACTCA 234
Qy      241 CAGTTCTTCAATGAACAGCTGAGAGTGAAGGACAGGCTGTCTATTACTGTCCGAG 299
Db      235 CTGTATCTGCAATGAACAGCTGAGAGCCGAGGAGGAGGCGGCTGTGTATTACTGTCCGAG 293

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RESULT 11
US-10-324-493-15

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; Sequence 15, Application US/10324493
; Publication No. US20030124121A1
; GENERAL INFORMATION:
; APPLICANT: Plueneke, John
; TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 3005-C
; CURRENT APPLICATION NUMBER: US/10/324,493
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/847,816
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/579,808
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/665,343
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/785,934
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 15
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: {1}..(348)
US-10-324-493-15

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Query Match      61.9%; Score 219; DB 15; Length 348;
Best Local Similarity 78.8%; Pred. No. 2.7e-59;
Matches 277; Conservative 0; Mismatches 70; Indels 6; Gaps 1;

Qy      2 AGGTGCGAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCT 61
Db      2 AGGTGCGAGCTGGTGGAGTCTGGGGGAGGCTGGTCCAGCTGGGAGGTCCCTGAGACTCT 61
Qy      62 CTTGCGAGCTCCGGGTTCAGGTTCACCTTCAATACTACTACAGTGGTCCGCC 121
Db      62 CTTGTTCCAGGCTCTG-----GATTCACTTCACTAGTAGTATGCGATGCACTGGTCCGCC 115
Qy      122 AGGTCCAGGCGAGGCGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTATCCCA 181
Db      116 AGGTCCAGGCGAGGCGCTGGAGTGGGTGGCAATTATATGTTTGAAGGAATAATCAAT 175
Qy      182 GGTACGAGACTCCGTGAAGGCGAGATTCACATCTCCAGAGAGAGCCCAACACAC 241
Db      176 ACTATGCGAGACTCCGTGAAGGCGGATTCACCTCTCCAGAGCAATTCACAGAACACGC 235
Qy      242 TGTTCCTTCAATGAACAGCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTCCGAGCT 301
Db      236 TGTATCTGGAATGAACAGCTGAGAGCCGAGGACAGCGCTGTGTATTACTGTCCGAGAG 295
Qy      302 TGACTACAGGCTCTGACTCTCTGGGGCGAGGAGTCTGGTCCAGCTCTCTCA 354
Db      296 GGAAGTACTACTTTGACTACTCTGGGGCGAGGAAACCTGGTCCAGCGTCTCTCA 348

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```

RESULT 12
US-10-324-493-11
; Sequence 11, Application US/10324493
; Publication No. US20030124121A1
; GENERAL INFORMATION:
; APPLICANT: Plueneke, John
; TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 3005-C
; CURRENT APPLICATION NUMBER: US/10/324,493
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/847,816
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/579,808
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/665,343
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/785,934

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;; PRIOR FILING DATE: 2001-02-15
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 11
;; LENGTH: 345
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; NAME/KEY: CDS
;; LOCATION: (1)..(345)
US-10-324-493-11

Query Match 61.7%; Score 218.4; DB 15; Length 345;
Best Local Similarity 80.2%; Pred. No. 4.2e-59;
Matches 284; Conservative 0; Mismatches 61; Indels 9; Gaps 2;

QY 1 GAGTGCAGCTGTCAGGTCCTGGGGCGGCTTGGCAAAAGCCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGTGCAGGTCGTCAGGTCGGGGGAAACCTTGGTACAGCCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCCTCCGGGTTTCAGGTTTCACTTCAATAAATCTACTATGAGTCTGGGTCCGC 120
DB 61 TCCTGCGCAGCCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCACCTATTTAGTGTAGTGTGATCCCA 180
DB 115 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCTTCTTATTTAGTGTAGTGTGATCCCA 174
QY 181 TGGTACGACAGCTCCGTTGAAGGCGAGATTCACTATCTCCAGAGAGAACCCCAACACACA 240
DB 175 TACTACGACAGCTCCGTTGAAGGCGGTTTCACTATCTCCAGAGACAATTCACAGACAGC 234
QY 241 CTGTTTCTTCAATGAACAGCCTGAGCTGAGGACAGGCTGTCTATTACTGTGCGAGC 300
DB 235 CTGTTATCTGCAAAATGAACAGCCTGAGGCGGAGGACACCGGCCATTTTTTACTGTGCGAAA 294
QY 301 TTGACTACAGC---GTCTGACTCTCTGGGCGCAGGAGTCTTGGTCAACCGTCTCTCTCA 354
DB 295 GATACACCGGGGATTTCTTCACTATTGGGGCCAGGGAACCTGGTCAACCGTCTCTCTCA 351

RESULT 14
US-10-460-595-1
;; Sequence 1, Application US/10460595
;; Publication No. US20040067532A1
;; GENERAL INFORMATION:
;; APPLICANT: Zhu, Li
;; APPLICANT: Wei, Shuanghong
;; APPLICANT: Hua, Shaobing
;; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION AND AFFINITY MATURATION OF HUMANIZED
;; FILE REFERENCE: 25636-730
;; CURRENT APPLICATION NUMBER: US/10/460,595
;; CURRENT FILING DATE: 2003-06-11
;; PRIOR APPLICATION NUMBER: US 60/403,296
;; PRIOR FILING DATE: 2002-08-12
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1
;; LENGTH: 296
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Consensus human germline VH sequence (DP47)
US-10-460-595-1

Query Match 61.2%; Score 216.8; DB 13; Length 296;
Best Local Similarity 85.6%; Pred. No. 1.3e-58;
Matches 255; Conservative 0; Mismatches 37; Indels 6; Gaps 1;

QY 1 GAGTGCAGCTGTCGAGTCTGGGGCGGCTTGGCAAAAGCCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGTGCAGCTGTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCCTCCGGGTTTCAGGTTTCACTTCAATAAATCTACTATGAGTCTGGGTCCGC 120
DB 61 TCCTGCGCAGCCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGTCTGGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCACCTATTTAGTGTAGTGTGATCCCA 180
DB 115 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCTCAGCTATTAGTGTAGTGTGATCCCA 174
QY 181 TGGTACGACAGCTCCGTTGAAGGCGAGATTCACTATCTCCAGAGAGAACCCCAACACACA 240
DB 175 TACTACGACAGCTCCGTTGAAGGCGGTTTCACTATCTCCAGAGACAATTCACAGACAGC 234
QY 241 CTGTTTCTTCAAAATGAACAGCCTGAGCTGAGGACAGGCTGTCTATTACTGTGCGAA 298
DB 235 CTGTTATCTGCAAAATGAACAGCCTGAGGCGGAGGACACCGGCCGTATATTACTGTGCGA 292

;; PRIOR FILING DATE: 2001-02-15
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 11
;; LENGTH: 345
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; NAME/KEY: CDS
;; LOCATION: (1)..(345)
US-10-324-493-11

Query Match 61.7%; Score 218.4; DB 15; Length 345;
Best Local Similarity 80.2%; Pred. No. 4.2e-59;
Matches 284; Conservative 0; Mismatches 61; Indels 9; Gaps 2;

QY 1 GAGTGCAGCTGTCAGGTCCTGGGGCGGCTTGGCAAAAGCCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGTGCAGGTCGTCAGGTCGGGGGAAACCTTGGTACAGCCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCCTCCGGGTTTCAGGTTTCACTTCAATAAATCTACTATGAGTCTGGGTCCGC 120
DB 61 TCCTGCGCAGCCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCACCTATTTAGTGTAGTGTGATCCCA 180
DB 115 CAGGCTCCAGGGCAGGGGCTGAGTGGGTCTCTTCTTATTTAGTGTAGTGTGATCCCA 171
QY 181 TGGTACGACAGCTCCGTTGAAGGCGAGATTCACTATCTCCAGAGAGAACCCCAACACACA 240
DB 172 AACTATGACAGCTCCGTTGAAGGCGGCTTCACTATCTCCAGAGACAATTCACAGACAGC 231
QY 241 CTGTTTCTTCAATGAACAGCCTGAGCTGAGGACAGGCTGTCTATTACTGTGCGAGC 300
DB 232 TTGTTATCTTCAATGAACAGCCTGAGGCGGAGGACACCGGCCATTTTTTACTGTGCGAAA 291
QY 301 TTGACTACAGGTCCTGACTCTCTGGGCGCAGGAGTCTTGGTCAACCGTCTCTCTCA 354
DB 292 GGGAGGTACTACTTTGACTACTGGGGCCAGGGAACCTGGTCAACCGTCTCTCTCA 345

RESULT 13
US-10-324-493-23
;; Sequence 23, Application US/10324493
;; Publication No. US20030124121A1
;; GENERAL INFORMATION:
;; APPLICANT: Pluenneke, John
;; TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF
;; FILE REFERENCE: 3005-C
;; CURRENT APPLICATION NUMBER: US/10/324,493
;; CURRENT FILING DATE: 2002-12-19
;; PRIOR APPLICATION NUMBER: US/09/847,816
;; PRIOR FILING DATE: 2001-05-01
;; PRIOR APPLICATION NUMBER: 09/579,808
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 09/665,343
;; PRIOR FILING DATE: 2000-09-19
;; PRIOR APPLICATION NUMBER: 09/785,934
;; PRIOR FILING DATE: 2001-02-15
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 23
;; LENGTH: 351
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(351)
US-10-324-493-23

Query Match 61.6%; Score 218.2; DB 15; Length 351;
Best Local Similarity 79.8%; Pred. No. 4.8e-59;
Matches 285; Conservative 0; Mismatches 63; Indels 9; Gaps 2;

RESULT 15
US-10-038-591-31
; Sequence 31, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-591-31

Query Match 61.2%; Score 216.8; DB 17; Length 296;
Best Local Similarity 85.6%; Pred. No. 1.3e-58;
Matches 255; Conservative 0; Mismatches 37; Indels 6; Gaps 1;
QY 1 GAGGTGCAGTGGTGGAGTCTGGGGGGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGCAGTGGTGGAGTCTGGGGGGGCTTGGTACAGCCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCCTCGGGGTTCAAGTTCACTTCAATAACTACTATGAGACTGGGTCCGC 120
Db 61 TCCTGTCAGCCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTATCCCA 180
Db 115 CAGGCTCCAGGGAGAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGCACA 174
QY 181 TGGTACGCGAGACTCCGTGAAGGGCAGATTTCACCATCTCCAGAGAGAACGCCAACACACA 240
Db 175 TACTACGCGAGACTCCGTGAAGGGCCCGTTTCAACATCTCCAGAGACATTTCCAGAACACAG 234
QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA 298
Db 235 CTGTATCTGCAANTGAACAGCTGAGAGCCGAGAGGACACGGCCGTATATTACTGTGCGA 292

Search completed: June 19, 2004, 10:06:38
Job time : 287 secs